

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Ser | Asp | Cys | Ile | Phe | Lys | Lys | Glu | Gln | Ala | Met | Cys | Leu | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

|         |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser     | Ser | Pro | Gly | Cys | Pro | Gly | Met | Trp | Asp | Asn | Ile | Thr | Cys | Trp | Lys |
| 1       |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro Ala |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Glu | Met | Val | Leu | Val | Ser | Cys | Pro | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Arg | Ile | Phe | Asn | Pro | Asp | Gln | Val | Trp | Glu | Thr | Glu | Thr | Ile | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Asn | Cys | Thr | Glu | Asp | Gly | Trp | Ser | Glu | Pro | Phe | Pro | His | Tyr | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

  

|     |     |     |     |     |
|-----|-----|-----|-----|-----|
| Asp | Ala | Cys | Gly | Phe |
|     |     |     | 20  |     |

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Gln | Asp | Tyr | Tyr | Tyr | Leu | Ser | Val | Lys | Ala | Leu | Tyr | Thr | Val | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

  

|     |     |     |     |     |
|-----|-----|-----|-----|-----|
| Tyr | Ser | Thr | Ser | Leu |
|     |     |     | 20  |     |

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Leu | Thr | Thr | Ala | Met | Val | Ile | Leu | Cys | Arg | Phe | Arg | Lys | Leu | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Cys | Thr | Arg | Asn | Phe | Ile | His | Met | Asn | Leu | Phe | Val | Ser | Phe | Met | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Ala | Ile | Ser | Val | Phe | Ile | Lys | Asp | Trp | Ile | Leu | Tyr | Ala | Glu | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     | 50  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Thr | Val | Glu | Cys | Lys | Ala | Val | Met | Val | Phe | Phe | His | Tyr | Cys | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Ser | Asn | Tyr | Phe | Trp | Leu | Phe | Ile | Glu | Gly | Leu | Tyr | Leu | Phe | Thr |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Leu | Val | Glu | Thr | Phe | Phe | Pro | Glu | Arg | Arg | Tyr | Phe | Tyr | Trp | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Ile | Ile | Gly | Trp | Gly | Thr | Pro | Thr | Val | Cys | Val |     |     |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Thr Ala Leu Trp Trp Val Ile Lys Gly Pro Val Val Gly Ser Ile Met  
 1 5 10 15  
 Val Asn Phe Val Leu Phe Ile Gly Ile Ile  
 20 25

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met Gly Gly Asn Glu Ser  
 1 5 10 15  
 Ser Ile Tyr

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 76 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile  
 1 5 10 15

His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys Arg Glu  
 20 25 30  
 Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val  
 35 40 45  
 Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu Ile Lys  
 50 55 60  
 Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe  
 65 70 75

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly  
 1 5 10 15  
 Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met  
 20 25 30  
 Ser

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu  
 1 5 10 15  
 Lys Ile Gln Arg Val Asn Asp Leu Met Gly Leu Asn Asp  
 20 25

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | His | Ser | Asp | Cys | Ile | Phe | Lys | Lys | Glu | Gln | Ala | Met | Cys | Leu | Glu | 1   | 5   | 10  | 15 |
| Lys | Ile | Gln | Arg | Val | Asn | Asp | Leu | Met | Gly | Leu | Asn | Asp | Ser | Ser | Pro | 20  | 25  | 30  |    |
| Gly | Cys | Pro | Gly | Met | Trp | Asp | Asn | Ile | Thr | Cys | Trp | Lys | Pro | Ala | His | 35  | 40  | 45  |    |
| Val | Gly | Glu | Met | Val | Leu | Val | Ser | Cys | Pro | Glu | Leu | Phe | Arg | Ile | Phe | 50  | 55  | 60  |    |
| Asn | Pro | Asp | Gln | Val | Trp | Glu | Thr | Glu | Thr | Ile | Gly | Glu | Phe | Gly | Phe | 65  | 70  | 75  |    |
| Ala | Asp | Ser | Lys | Ser | Leu | Asp | Leu | Ser | Asp | Met | Arg | Val | Val | Ser | Arg | 85  | 90  | 95  |    |
| Asn | Cys | Thr | Glu | Asp | Gly | Trp | Ser | Glu | Pro | Phe | Pro | His | Tyr | Phe | Asp | 100 | 105 | 110 |    |
| Ala | Cys | Gly | Phe | Glu | Glu | Tyr | Glu | Ser | Glu | Thr | Gly | Asp | Gln | Asp | Tyr | 115 | 120 | 125 |    |
| Tyr | Tyr | Leu | Ser | Val | Lys | Ala | Leu | Tyr | Thr | Val | Gly | Tyr | Ser | Thr | Ser | 130 | 135 | 140 |    |
| Leu | Val | Thr | Leu | Thr | Thr | Ala | Met | Val | Ile | Leu | Cys | Arg | Phe | Arg | Lys | 145 | 150 | 155 |    |
| Leu | His | Cys | Thr | Arg | Asn | Phe | Ile | His | Met | Asn | Leu | Phe | Val | Ser | Phe | 165 | 170 | 175 |    |
| Met | Leu | Arg | Ala | Ile | Ser | Val | Phe | Ile | Lys | Asp | Trp | Ile | Leu | Tyr | Ala | 180 | 185 | 190 |    |
| Glu | Gln | Asp | Ser | Asn | His | Cys | Phe | Val | Ser | Thr | Val | Glu | Cys | Lys | Ala | 195 | 200 | 205 |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Met | Val | Phe | Phe | His | Tyr | Cys | Val | Val | Ser | Asn | Tyr | Phe | Trp | Leu |
| 210 |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Ile | Glu | Gly | Leu | Tyr | Leu | Phe | Thr | Leu | Leu | Val | Glu | Thr | Phe | Phe |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Pro | Glu | Arg | Arg | Tyr | Phe | Tyr | Trp | Tyr | Ile | Ile | Ile | Gly | Trp | Gly | Thr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Pro | Thr | Val | Cys | Val | Ser | Val | Trp | Ala | Met | Leu | Arg | Leu | Tyr | Phe | Asp |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asp | Thr | Gly | Cys | Trp | Asp | Met | Asn | Asp | Asn | Thr | Ala | Leu | Trp | Trp | Val |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile | Lys | Gly | Pro | Val | Val | Gly | Ser | Ile | Met | Val | Asn | Phe | Val | Leu | Phe |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ile | Gly | Ile | Ile | Val | Ile | Leu | Val | Gln | Lys | Leu | Gln | Ser | Pro | Asp | Met |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Gly | Gly | Asn | Glu | Ser | Ser | Ile | Tyr | Phe | Ser | Cys | Val | Gln | Lys | Cys | Tyr |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Cys | Lys | Pro | Gln | Arg | Ala | Gln | Gln | His | Ser | Cys | Lys | Met | Ser | Glu | Leu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ser | Thr | Ile | Thr | Leu | Arg | Leu | Ala | Arg | Ser | Thr | Leu | Leu | Leu | Ile | Pro |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Leu | Phe | Gly | Ile | His | Tyr | Thr | Val | Phe | Ala | Phe | Ser | Pro | Glu | Asn | Val |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Ser | Lys | Arg | Glu | Arg | Leu | Val | Phe | Glu | Leu | Gly | Leu | Gly | Ser | Phe | Gln |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Gly | Phe | Val | Val | Ala | Val | Leu | Tyr | Cys | Phe | Leu | Asn | Gly | Glu | Val | Gln |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Ala | Glu | Ile | Lys | Arg | Lys | Trp | Arg | Ser | Trp | Lys | Val | Asn | Arg | Tyr | Phe |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Thr | Met | Asp | Phe | Lys | His | Arg | His | Pro | Ser | Leu | Ala | Ser | Ser | Gly | Val |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Asn | Gly | Gly | Thr | Gln | Leu | Ser | Ile | Leu | Ser | Lys | Ser | Ser | Ser | Gln | Ile |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Arg | Met | Ser | Gly | Leu | Pro | Ala | Asp | Asn | Leu | Ala | Thr |     |     |     |     |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Arg Gly Gly Arg His Trp Pro Glu Pro Pro Cys Arg Leu Arg Ser  
1 5 10 15

Val Met Ala Ser Ile Ala Gln Val Ser Leu Ala Ala Leu Leu Leu Leu  
20 25 30

Pro Met Ala Thr Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln  
35 40 45

Ala Met Cys Leu Glu Lys Ile Gln Arg Val Asn Asp Leu Met Gly Leu  
50 55 60

Asn Asp Ser Ser Pro Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys  
65 70 75 80

Trp Lys Pro Ala His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu  
85 90 95

Leu Phe Arg Ile Phe Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile  
 : 100 105 110

Gly Glu Phe Gly Phe Ala Asp Ser Lys Ser Leu Asp Leu Ser Asp Met  
115 120 125

Arg Val Val Ser Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro-Phe  
130 135 140

Pro His Tyr Phe Asp Ala Cys Gly Phe Glu Glu Tyr Glu Ser Glu Thr  
145 150 155 160

Gly Asp Gln Asp Tyr Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val  
165 170 175

Gly Tyr Ser Thr Ser Leu Val Thr Leu Thr Thr Ala Met Val Ile Leu  
180 185 190

Cys Arg Phe Arg Lys Leu His Cys Thr Arg Asn Phe Ile His Met Asn  
195 200 205

Leu Phe Val Ser Phe Met Leu Arg Ala Ile Ser Val Phe Ile Lys Asp  
210 215 220

**Q**uestions are asked about the following:



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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Ile | Leu | Tyr | Ala | Glu | Gln | Asp | Ser | Asn | His | Cys | Phe | Val | Ser | Thr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Val | Glu | Cys | Lys | Ala | Val | Met | Val | Phe | Phe | His | Tyr | Cys | Val | Val | Ser |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asn | Tyr | Phe | Trp | Leu | Phe | Ile | Glu | Gly | Leu | Tyr | Leu | Phe | Thr | Leu | Leu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Glu | Thr | Phe | Phe | Pro | Glu | Arg | Arg | Tyr | Phe | Tyr | Trp | Tyr | Ile | Ile |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile | Gly | Trp | Gly | Thr | Pro | Thr | Val | Cys | Val | Ser | Val | Trp | Ala | Met | Leu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Arg | Leu | Tyr | Phe | Asp | Asp | Thr | Gly | Cys | Trp | Asp | Met | Asn | Asp | Asn | Thr |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Ala | Leu | Trp | Trp | Val | Ile | Lys | Gly | Pro | Val | Val | Gly | Ser | Ile | Met | Val |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Asn | Phe | Val | Leu | Phe | Ile | Gly | Ile | Ile | Val | Ile | Leu | Val | Gln | Lys | Leu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Gln | Ser | Pro | Asp | Met | Gly | Gly | Asn | Glu | Ser | Ser | Ile | Tyr | Phe | Ser | Cys |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Val | Gln | Lys | Cys | Tyr | Cys | Lys | Pro | Gln | Arg | Ala | Gln | Gln | His | Ser | Cys |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Lys | Met | Ser | Glu | Leu | Ser | Thr | Ile | Thr | Leu | Arg | Leu | Ala | Arg | Ser | Thr |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Leu | Leu | Leu | Ile | Pro | Leu | Phe | Gly | Ile | His | Tyr | Thr | Val | Phe | Ala | Phe |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Ser | Pro | Glu | Asn | Val | Ser | Lys | Arg | Glu | Arg | Leu | Val | Phe | Glu | Leu | Gly |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Leu | Gly | Ser | Phe | Gln | Gly | Phe | Val | Val | Ala | Val | Leu | Tyr | Cys | Phe | Leu |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Asn | Gly | Glu | Val | Gln | Ala | Glu | Ile | Lys | Arg | Lys | Trp | Arg | Ser | Trp | Lys |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Val | Asn | Arg | Tyr | Phe | Thr | Met | Asp | Phe | Lys | His | Arg | His | Pro | Ser | Leu |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Ala | Ser | Ser | Gly | Val | Asn | Gly | Gly | Thr | Gln | Leu | Ser | Ile | Leu | Ser | Lys |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Ser | Ser | Ser | Gln | Ile | Arg | Met | Ser | Gly | Leu | Pro | Ala | Asp | Asn | Leu | Ala |

500

505

510

Thr

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu  
1 5 10 15

Lys Ile Gln Arg Val Asn Asp Leu Met Gly Leu Asn Asp Ser Ser Pro  
20 25 30

Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala His  
35 40 45

Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile Phe  
50 55 60

Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Phe Gly Phe  
65 70 75 80

Ala Asp Ser Lys Ser Leu Asp Leu Ser Asp Met Arg Val Val Ser Arg  
85 90 95

Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe Asp  
100 105 110

Ala Cys Gly Phe Glu Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr  
115 120 125

Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser  
130 135 140

Leu Val Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys  
145 150 155 160

Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe  
165 170 175

Met Leu Arg Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala

| 180 |     |     |     |     |     |     |     |     |     | 185 |     |     |     | 190 |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Glu | Gln | Asp | Ser | Asn | His | Cys | Phe | Val | Ser | Thr | Val | Glu | Cys | Lys | Ala |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |
| Val | Met | Val | Phe | Phe | His | Tyr | Cys | Val | Val | Ser | Asn | Tyr | Phe | Trp | Leu |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |
| Phe | Ile | Glu | Gly | Leu | Tyr | Leu | Phe | Thr | Leu | Leu | Val | Glu | Thr | Phe | Phe |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |
| Pro | Glu | Arg | Arg | Tyr | Phe | Tyr | Trp | Tyr | Ile | Ile | Ile | Gly | Trp | Gly | Thr |  |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |
| Pro | Thr | Val | Cys | Val | Ser | Val | Trp | Ala | Met | Leu | Arg | Leu | Tyr | Phe | Asp |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |
| Asp | Thr | Gly | Cys | Trp | Asp | Met | Asn | Asp | Asn | Thr | Ala | Leu | Trp | Trp | Val |  |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |
| Ile | Lys | Gly | Pro | Val | Val | Gly | Ser | Ile | Met | Val | Asn | Phe | Val | Leu | Phe |  |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |
| Ile | Gly | Ile | Ile | Val | Ile | Leu | Val | Gln | Lys | Leu | Gln | Ser | Pro | Asp | Met |  |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |  |
| Gly | Gly | Asn | Glu | Ser | Ser | Ile | Tyr | Leu | Arg | Leu | Ala | Arg | Ser | Thr | Leu |  |  |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |  |
| Leu | Leu | Ile | Pro | Leu | Phe | Gly | Ile | His | Tyr | Thr | Val | Phe | Ala | Phe | Ser |  |  |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |  |
| Pro | Glu | Asn | Val | Ser | Lys | Arg | Glu | Arg | Leu | Val | Phe | Glu | Leu | Gly | Leu |  |  |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |  |
| Gly | Ser | Phe | Gln | Gly | Phe | Val | Val | Ala | Val | Leu | Tyr | Cys | Phe | Leu | Asn |  |  |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |  |
| Gly | Glu | Val | Gln | Ala | Glu | Ile | Lys | Arg | Lys | Trp | Arg | Ser | Trp | Lys | Val |  |  |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |  |  |
| Asn | Arg | Tyr | Phe | Thr | Met | Asp | Phe | Lys | His | Arg | His | Pro | Ser | Leu | Ala |  |  |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |  |  |
| Ser | Ser | Gly | Val | Asn | Gly | Gly | Thr | Gln | Leu | Ser | Ile | Leu | Ser | Lys | Ser |  |  |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |  |
| Ser | Ser | Gln | Ile | Arg | Met | Ser | Gly | Leu | Pro | Ala | Asp | Asn | Leu | Ala | Thr |  |  |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |  |  |

160

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Arg | Gly | Gly | Arg | His | Trp | Pro | Glu | Pro | Pro | Cys | Arg | Leu | Arg | Ser | 1   | 5   | 10  | 15 |
| Val | Met | Ala | Ser | Ile | Ala | Gln | Val | Ser | Leu | Ala | Ala | Leu | Leu | Leu | Leu | 20  | 25  | 30  |    |
| Pro | Met | Ala | Thr | Ala | Met | His | Ser | Asp | Cys | Ile | Phe | Lys | Lys | Glu | Gln | 35  | 40  | 45  |    |
| Ala | Met | Cys | Leu | Glu | Lys | Ile | Gln | Arg | Val | Asn | Asp | Leu | Met | Gly | Leu | 50  | 55  | 60  |    |
| Asn | Asp | Ser | Ser | Pro | Gly | Cys | Pro | Gly | Met | Trp | Asp | Asn | Ile | Thr | Cys | 65  | 70  | 75  |    |
| Trp | Lys | Pro | Ala | His | Val | Gly | Glu | Met | Val | Leu | Val | Ser | Cys | Pro | Glu | 85  | 90  | 95  |    |
| Leu | Phe | Arg | Ile | Phe | Asn | Pro | Asp | Gln | Val | Trp | Glu | Thr | Glu | Thr | Ile | 100 | 105 | 110 |    |
| Gly | Glu | Phe | Gly | Phe | Ala | Asp | Ser | Lys | Ser | Leu | Asp | Leu | Ser | Asp | Met | 115 | 120 | 125 |    |
| Arg | Val | Val | Ser | Arg | Asn | Cys | Thr | Glu | Asp | Gly | Trp | Ser | Glu | Pro | Phe | 130 | 135 | 140 |    |
| Pro | His | Tyr | Phe | Asp | Ala | Cys | Gly | Phe | Glu | Glu | Tyr | Glu | Ser | Glu | Thr | 145 | 150 | 155 |    |
| Gly | Asp | Gln | Asp | Tyr | Tyr | Tyr | Leu | Ser | Val | Lys | Ala | Leu | Tyr | Thr | Val | 165 | 170 | 175 |    |
| Gly | Tyr | Ser | Thr | Ser | Leu | Val | Thr | Leu | Thr | Thr | Ala | Met | Val | Ile | Leu | 180 | 185 | 190 |    |
| Cys | Arg | Phe | Arg | Lys | Leu | His | Cys | Thr | Arg | Asn | Phe | Ile | His | Met | Asn | 195 | 200 | 205 |    |
| Leu | Phe | Val | Ser | Phe | Met | Leu | Arg | Ala | Ile | Ser | Val | Phe | Ile | Lys | Asp | 210 | 215 | 220 |    |

Asp Asn Leu Ala Thr  
485

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp Leu  
210 215 220

Phe Ile Glu Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe  
 225 230 235 240  
 Pro Glu Arg Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly Thr  
 245 250 255  
 Pro Thr Val Cys Val Thr Val Trp Ala Val Leu Arg Leu Tyr Phe Asp  
 260 265 270  
 Asp Ala Gly Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp Val  
 275 280 285  
 Ile Lys Gly Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu Phe  
 290 295 300  
 Ile Gly Ile Ile Ile Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met  
 305 310 315 320  
 Gly Gly Asn Glu Ser Ser Ile Tyr Leu Arg Leu Ala Arg Ser Thr Leu  
 325 330 335  
 Leu Leu Ile Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser  
 340 345 350  
 Pro Glu Asn Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu  
 355 360 365  
 Gly Ser Phe Gln Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn  
 370 375 380  
 Gly Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val  
 385 390 395 400  
 Asn Arg Tyr Phe Thr Met Asp Phe Lys His Arg His Pro Ser Leu Ala  
 405 410 415  
 Ser Ser Gly Val Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser  
 420 425 430  
 Ser Ser Gln Leu Arg Met Ser Ser Leu Pro Ala Asp Asn Leu Ala Thr  
 435 440 445

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

[illegible]

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Arg | Val | Leu | Gln | Leu | Ser | Leu | Thr | Ala | Leu | Leu | Leu | Pro | Val | 1   | 5   | 10  | 15  |
| Ala | Ile | Ala | Met | His | Ser | Asp | Cys | Ile | Phe | Lys | Lys | Glu | Gln | Ala | Met | 20  | 25  | 30  |     |
| Cys | Leu | Glu | Arg | Ile | Gln | Arg | Ala | Asn | Asp | Leu | Met | Gly | Leu | Asn | Glu | 35  | 40  | 45  |     |
| Ser | Ser | Pro | Gly | Cys | Pro | Gly | Met | Trp | Asp | Asn | Ile | Thr | Cys | Trp | Lys | 50  | 55  | 60  |     |
| Pro | Ala | Gln | Val | Gly | Glu | Met | Val | Leu | Val | Ser | Cys | Pro | Glu | Val | Phe | 65  | 70  | 75  | 80  |
| Arg | Ile | Phe | Asn | Pro | Asp | Gln | Val | Trp | Met | Thr | Glu | Thr | Ile | Gly | Asp | 85  | 90  | 95  |     |
| Ser | Gly | Phe | Ala | Asp | Ser | Asn | Ser | Leu | Glu | Ile | Thr | Asp | Met | Gly | Val | 100 | 105 | 110 |     |
| Val | Gly | Arg | Asn | Cys | Thr | Glu | Asp | Gly | Trp | Ser | Glu | Pro | Phe | Pro | His | 115 | 120 | 125 |     |
| Tyr | Phe | Asp | Ala | Cys | Gly | Phe | Asp | Asp | Tyr | Glu | Pro | Glu | Ser | Gly | Asp | 130 | 135 | 140 |     |
| Gln | Asp | Tyr | Tyr | Tyr | Leu | Ser | Val | Lys | Ala | Leu | Tyr | Thr | Val | Gly | Tyr | 145 | 150 | 155 | 160 |
| Ser | Thr | Ser | Leu | Ala | Thr | Leu | Thr | Thr | Ala | Met | Val | Ile | Leu | Cys | Arg | 165 | 170 | 175 |     |
| Phe | Arg | Lys | Leu | His | Cys | Thr | Arg | Asn | Phe | Ile | His | Met | Asn | Leu | Phe | 180 | 185 | 190 |     |
| Val | Ser | Phe | Met | Leu | Arg | Ala | Ile | Ser | Val | Phe | Ile | Lys | Asp | Trp | Ile | 195 | 200 | 205 |     |
| Leu | Tyr | Ala | Glu | Gln | Asp | Ser | Ser | His | Cys | Phe | Val | Ser | Thr | Val | Glu | 210 | 215 | 220 |     |
| Cys | Lys | Ala | Val | Met | Val | Phe | Phe | His | Tyr | Cys | Val | Val | Ser | Asn | Tyr | 225 | 230 | 235 | 240 |
| Phe | Trp | Leu | Phe | Ile | Glu | Gly | Leu | Tyr | Leu | Phe | Thr | Leu | Leu | Val | Glu | 245 | 250 | 255 |     |
| Thr | Phe | Phe | Pro | Glu | Arg | Arg | Tyr | Phe | Tyr | Trp | Tyr | Thr | Ile | Ile | Gly |     |     |     |     |



|   |     |     |
|---|-----|-----|
| 260   | 265 | 270 |
| Trp Gly Thr Pro Thr Val Cys Val Thr Val Trp Ala Val Leu Arg Leu |     |     |
| 275   | 280 | 285 |
| Tyr Phe Asp Asp Ala Gly Cys Trp Asp Met Asn Asp Ser Thr Ala Leu |     |     |
| 290   | 295 | 300 |
| Trp Trp Val Ile Lys Gly Pro Val Val Gly Ser Ile Met Val Asn Phe |     |     |
| 305   | 310 | 315 |
| Val Leu Phe Ile Gly Ile Ile Ile Ile Leu Val Gln Lys Leu Gln Ser |     |     |
|   | 325 | 330 |
| Pro Asp Met Gly Gly Asn Glu Ser Ser Ile Tyr Leu Arg Leu Ala Arg |     |     |
|   | 340 | 345 |
| Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile His Tyr Thr Val Phe |     |     |
|   | 355 | 360 |
| Ala Phe Ser Pro Glu Asn Val Ser Lys Arg Glu Arg Leu Val Phe Glu |     |     |
|   | 370 | 375 |
| Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val Ala Val Leu Tyr Cys |     |     |
|   | 385 | 390 |
| Phe Leu Asn Gly Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser |     |     |
|   | 405 | 410 |
| Trp Lys Val Asn Arg Tyr Phe Thr Met Asp Phe Lys His Arg His Pro |     |     |
|   | 420 | 425 |
| Ser Leu Ala Ser Ser Gly Val Asn Gly Gly Thr Gln Leu Ser Ile Leu |     |     |
|   | 435 | 440 |
| Ser Lys Ser Ser Ser Gln Leu Arg Met Ser Ser Leu Pro Ala Asp Asn |     |     |
|   | 450 | 455 |
| Leu Ala Thr   |     |     |
| 465   |     |     |

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met<br>1   | His        | Ser        | Asp<br>5   | Cys<br>5   | Ile        | Phe        | Lys        | Lys        | Glu<br>10  | Gln        | Ala        | Met        | Cys        | Leu<br>15  | Glu        |
| Arg        | Ile        | Gln<br>20  | Arg<br>20  | Ala        | Asn        | Asp        | Leu        | Met<br>25  | Gly        | Leu        | Asn        | Glu        | Ser<br>30  | Ser        | Pro        |
| Gly        | Cys        | Pro<br>35  | Gly        | Met        | Trp        | Asp        | Asn<br>40  | Ile        | Thr        | Cys        | Trp        | Lys<br>45  | Pro        | Ala        | Gln        |
| Val<br>50  | Gly<br>50  | Glu        | Met        | Val        | Leu        | Val<br>55  | Ser        | Cys        | Pro        | Glu        | Val<br>60  | Phe        | Arg        | Ile        | Phe        |
| Asn<br>65  | Pro        | Asp        | Gln        | Val        | Trp<br>70  | Met        | Thr        | Glu        | Thr        | Ile<br>75  | Gly        | Asp        | Ser        | Gly        | Phe<br>80  |
| Ala        | Asp        | Ser        | Asn<br>85  | Ser<br>85  | Leu        | Glu        | Ile        | Thr<br>90  | Asp<br>90  | Met        | Gly        | Val        | Val        | Gly<br>95  | Arg        |
| Asn        | Cys        | Thr<br>100 | Glu<br>100 | Asp        | Gly        | Trp        | Ser        | Glu<br>105 | Pro        | Phe        | Pro        | His        | Tyr<br>110 | Phe        | Asp        |
| Ala        | Cys        | Gly<br>115 | Phe        | Asp        | Asp        | Tyr        | Glu<br>120 | Pro        | Glu        | Ser        | Gly        | Asp<br>125 | Gln        | Asp        | Tyr        |
| Tyr<br>130 | Tyr<br>130 | Leu        | Ser        | Val        | Lys        | Ala<br>135 | Leu        | Tyr        | Thr        | Val        | Gly<br>140 | Tyr        | Ser        | Thr        | Ser        |
| Leu<br>145 | Ala        | Thr        | Leu        | Thr        | Thr<br>150 | Ala        | Met        | Val        | Ile        | Leu<br>155 | Cys        | Arg        | Phe        | Arg        | Lys<br>160 |
| Leu        | His        | Cys        | Thr<br>165 | Arg<br>165 | Asn        | Phe        | Ile        | His<br>170 | Met<br>170 | Asn        | Leu        | Phe        | Val        | Ser<br>175 | Phe        |
| Met        | Leu        | Arg<br>180 | Ala<br>180 | Ile        | Ser        | Val        | Phe        | Ile<br>185 | Lys        | Asp        | Trp        | Ile        | Leu<br>190 | Tyr        | Ala        |
| Glu        | Gln        | Asp<br>195 | Ser        | Ser        | His        | Cys        | Phe<br>200 | Val        | Ser        | Thr        | Val        | Glu<br>205 | Cys        | Lys        | Ala        |
| Val<br>210 | Met<br>210 | Val        | Phe        | Phe        | His        | Tyr<br>215 | Cys        | Val        | Val        | Ser        | Asn<br>220 | Tyr        | Phe        | Trp        | Leu        |
| Phe<br>225 | Ile        | Glu        | Gly        | Leu        | Tyr<br>230 | Leu        | Phe        | Thr        | Leu        | Leu<br>235 | Val        | Glu        | Thr        | Phe        | Phe<br>240 |
| Pro        | Glu        | Arg        | Arg<br>245 | Tyr<br>245 | Phe        | Tyr        | Trp        | Tyr        | Thr<br>250 | Ile        | Ile        | Gly        | Trp        | Gly<br>255 | Thr        |
| Pro        | Thr        | Val        | Cys<br>260 | Val        | Thr        | Val        | Trp        | Ala<br>265 | Val        | Leu        | Arg        | Leu        | Tyr<br>270 | Phe        | Asp        |

Asp Ala Gly Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp Val  
 275 280 285  
 Ile Lys Gly Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu Phe  
 290 295 300  
 Ile Gly Ile Ile Ile Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met  
 305 310 315 320  
 Gly Gly Asn Glu Ser Ser Ile Tyr Phe Ser Cys Val Gln Lys Cys Tyr  
 325 330 335  
 Cys Lys Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu  
 340 345 350  
 Ser Thr Ile Thr Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro  
 355 360 365  
 Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val  
 370 375 380  
 Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln  
 385 390 395 400  
 Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln  
 405 410 415  
 Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe  
 420 425 430  
 Thr Met Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val  
 435 440 445  
 Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Leu  
 450 455 460  
 Arg Met Ser Ser Leu Pro Ala Asp Asn Leu Ala Thr  
 465 470 475

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Ala Arg Val Leu Gln Leu Ser Leu Thr Ala Leu Leu Leu Pro Val  
1 5 10 15

Ala Ile Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met  
20 25 30

Cys Leu Glu Arg Ile Gln Arg Ala Asn Asp Leu Met Gly Leu Asn Glu  
35 40 45

Ser Ser Pro Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys  
50 55 60

Pro Ala Gln Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Val Phe  
65 70 75 80

Arg Ile Phe Asn Pro Asp Gln Val Trp Met Thr Glu Thr Ile Gly Asp  
85 90 95

Ser Gly Phe Ala Asp Ser Asn Ser Leu Glu Ile Thr Asp Met Gly Val  
100 105 110

Val Gly Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His  
115 120 125

Tyr Phe Asp Ala Cys Gly Phe Asp Asp Tyr Glu Pro Glu Ser Gly Asp  
130 135 140

Gln Asp Tyr Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr  
145 150 155 160

Ser Thr Ser Leu Ala Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg  
165 170 175

Phe Arg Lys Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe  
180 185 190

Val Ser Phe Met Leu Arg Ala Ile Ser Val Phe Ile Lys Asp Trp Ile  
195 200 205

Leu Tyr Ala Glu Gln Asp Ser Ser His Cys Phe Val Ser Thr Val Glu  
210 215 220

Cys Lys Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn Tyr  
225 230 235 240

Phe Trp Leu Phe Ile Glu Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu  
245 250 255

Thr Phe Phe Pro Glu Arg Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly  
260 265 270

Trp Gly Thr Pro Thr Val Cys Val Thr Val Trp Ala Val Leu Arg Leu

| 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Phe | Asp | Asp | Ala | Gly | Cys | Trp | Asp | Met | Asn | Asp | Ser | Thr | Ala | Leu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Trp | Trp | Val | Ile | Lys | Gly | Pro | Val | Val | Gly | Ser | Ile | Met | Val | Asn | Phe |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Val | Leu | Phe | Ile | Gly | Ile | Ile | Ile | Ile | Leu | Val | Gln | Lys | Leu | Gln | Ser |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Pro | Asp | Met | Gly | Gly | Asn | Glu | Ser | Ser | Ile | Tyr | Phe | Ser | Cys | Val | Gln |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Lys | Cys | Tyr | Cys | Lys | Pro | Gln | Arg | Ala | Gln | Gln | His | Ser | Cys | Lys | Met |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ser | Glu | Leu | Ser | Thr | Ile | Thr | Leu | Arg | Leu | Ala | Arg | Ser | Thr | Leu | Leu |
|     |     |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Leu | Ile | Pro | Leu | Phe | Gly | Ile | His | Tyr | Thr | Val | Phe | Ala | Phe | Ser | Pro |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Glu | Asn | Val | Ser | Lys | Arg | Glu | Arg | Leu | Val | Phe | Glu | Leu | Gly | Leu | Gly |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Ser | Phe | Gln | Gly | Phe | Val | Val | Ala | Val | Leu | Tyr | Cys | Phe | Leu | Asn | Gly |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Glu | Val | Gln | Ala | Glu | Ile | Lys | Arg | Lys | Trp | Arg | Ser | Trp | Lys | Val | Asn |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Arg | Tyr | Phe | Thr | Met | Asp | Phe | Lys | His | Arg | His | Pro | Ser | Leu | Ala | Ser |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Ser | Gly | Val | Asn | Gly | Gly | Thr | Gln | Leu | Ser | Ile | Leu | Ser | Lys | Ser | Ser |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Ser | Gln | Leu | Arg | Met | Ser | Ser | Leu | Pro | Ala | Asp | Asn | Leu | Ala | Thr |     |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Ser | Asp | Cys | Ile | Phe | Lys | Lys | Glu | Gln | Ala | Met | Cys | Leu | Glu | 1   | 5   | 10  | 15  |
| Lys | Ile | Gln | Arg | Ala | Asn | Glu | Leu | Met | Gly | Phe | Asn | Asp | Ser | Ser | Pro | 20  | 25  | 30  |     |
| Gly | Cys | Pro | Gly | Met | Trp | Asp | Asn | Ile | Thr | Cys | Trp | Lys | Pro | Ala | His | 35  | 40  | 45  |     |
| Val | Gly | Glu | Met | Val | Leu | Val | Ser | Cys | Pro | Glu | Leu | Phe | Arg | Ile | Phe | 50  | 55  | 60  |     |
| Asn | Pro | Asp | Gln | Val | Trp | Glu | Thr | Glu | Thr | Ile | Gly | Glu | Ser | Asp | Phe | 65  | 70  | 75  | 80  |
| Gly | Asp | Ser | Asn | Ser | Leu | Asp | Leu | Ser | Asp | Met | Gly | Val | Val | Ser | Arg | 85  | 90  | 95  |     |
| Asn | Cys | Thr | Glu | Asp | Gly | Trp | Ser | Glu | Pro | Phe | Pro | His | Tyr | Phe | Asp | 100 | 105 | 110 |     |
| Ala | Cys | Gly | Phe | Asp | Glu | Tyr | Glu | Ser | Glu | Thr | Gly | Asp | Gln | Asp | Tyr | 115 | 120 | 125 |     |
| Tyr | Tyr | Leu | Ser | Val | Lys | Ala | Leu | Tyr | Thr | Val | Gly | Tyr | Ser | Thr | Ser | 130 | 135 | 140 |     |
| Leu | Val | Thr | Leu | Thr | Thr | Ala | Met | Val | Ile | Leu | Cys | Arg | Phe | Arg | Lys | 145 | 150 | 155 | 160 |
| Leu | His | Cys | Thr | Arg | Asn | Phe | Ile | His | Met | Asn | Leu | Phe | Val | Ser | Phe | 165 | 170 | 175 |     |
| Met | Leu | Arg | Ala | Ile | Ser | Val | Phe | Ile | Lys | Asp | Trp | Ile | Leu | Tyr | Ala | 180 | 185 | 190 |     |
| Glu | Gln | Asp | Ser | Asn | His | Cys | Phe | Ile | Ser | Thr | Val | Glu | Cys | Lys | Ala | 195 | 200 | 205 |     |
| Val | Met | Val | Phe | Phe | His | Tyr | Cys | Val | Val | Ser | Asn | Tyr | Phe | Trp | Leu | 210 | 215 | 220 |     |
| Phe | Ile | Glu | Gly | Leu | Tyr | Leu | Phe | Thr | Leu | Leu | Val | Glu | Thr | Phe | Phe | 225 | 230 | 235 | 240 |
| Pro | Glu | Arg | Arg | Tyr | Phe | Tyr | Trp | Tyr | Thr | Ile | Ile | Gly | Trp | Gly | Thr | 245 | 250 | 255 |     |
| Pro | Thr | Val | Cys | Val | Thr | Val | Trp | Ala | Thr | Leu | Arg | Leu | Tyr | Phe | Asp | 260 | 265 | 270 |     |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Thr | Gly | Cys | Trp | Asp | Met | Asn | Asp | Ser | Thr | Ala | Leu | Trp | Trp | Val |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile | Lys | Gly | Pro | Val | Val | Gly | Ser | Ile | Met | Val | Asn | Phe | Val | Leu | Phe |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ile | Gly | Ile | Ile | Val | Ile | Leu | Val | Gln | Lys | Leu | Gln | Ser | Pro | Asp | Met |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Gly | Gly | Asn | Glu | Ser | Ser | Ile | Tyr | Leu | Arg | Leu | Ala | Arg | Ser | Thr | Leu |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Leu | Leu | Ile | Pro | Leu | Phe | Gly | Ile | His | Tyr | Thr | Val | Phe | Ala | Phe | Ser |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Pro | Glu | Asn | Val | Ser | Lys | Arg | Glu | Arg | Leu | Val | Phe | Glu | Leu | Gly | Leu |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Gly | Ser | Phe | Gln | Gly | Phe | Val | Val | Ala | Val | Leu | Tyr | Cys | Phe | Leu | Asn |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Gly | Glu | Val | Gln | Ala | Glu | Ile | Lys | Arg | Lys | Trp | Arg | Ser | Trp | Lys | Val |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |     |
| Asn | Arg | Tyr | Phe | Ala | Val | Asp | Phe | Lys | His | Arg | His | Pro | Ser | Leu | Ala |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Ser | Ser | Gly | Val | Asn | Gly | Gly | Thr | Gln | Leu | Ser | Ile | Leu | Ser | Lys | Ser |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Ser | Ser | Gln | Ile | Arg | Met | Ser | Gly | Leu | Pro | Ala | Asp | Asn | Leu | Ala | Thr |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gly | Val | Val | His | Val | Ser | Leu | Ala | Ala | His | Cys | Gly | Ala | Cys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Trp | Gly | Arg | Gly | Arg | Leu | Arg | Lys | Gly | Arg | Ala | Ala | Cys | Lys | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu Leu Ser Val Gly  
35 40 45

Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly Val Val His Val  
50 55 60

Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Pro Ala Met His Ser  
65 70 75 80

Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu Lys Ile Gln  
85 90 95

Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser Pro Gly Cys Pro  
100 105 110

Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala His Val Gly Glu  
115 120 125

Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile Phe Asn Pro Asp  
130 135 140

Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp Phe Gly Asp Ser  
145 150 155 160

Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser Arg Asn Cys Thr  
165 170 175

Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe Asp Ala Cys Gly  
180 185 190

Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr Tyr Tyr Leu  
195 200 205

Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser Leu Val Thr  
210 215 220

Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys Leu His Cys  
225 230 235 240

Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe Met Leu Arg  
245 250 255

Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp  
260 265 270

Ser Asn His Cys Phe Ile Ser Thr Val Glu Cys Lys Ala Val Met Val  
275 280 285

Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp Leu Phe Ile Glu  
290 295 300

Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg



305                      310                      315                      320  
 Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly Thr Pro Thr Val  
                                  325                      330                      335  
 Cys Val Thr Val Trp Ala Thr Leu Arg Leu Tyr Phe Asp Asp Thr Gly  
                                  340                      345                      350  
 Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp Val Ile Lys Gly  
                                  355                      360                      365  
 Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu Phe Ile Gly Ile  
                                  370                      375                      380  
 Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met Gly Gly Asn  
                                  385                      390                      395                      400  
 Glu Ser Ser Ile Tyr Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile  
                                  405                      410                      415  
 Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn  
                                  420                      425                      430  
 Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe  
                                  435                      440                      445  
 Gln Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val  
                                  450                      455                      460  
 Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr  
                                  465                      470                      475                      480  
 Phe Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly  
                                  485                      490                      495  
 Val Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser-Gln  
                                  500                      505                      510  
 Ile Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr  
                                  515                      520                      525

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

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|            |     |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|-----|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met<br>1   | His | Ser        | Asp        | Cys<br>5   | Ile        | Phe        | Lys        | Lys        | Glu<br>10  | Gln        | Ala        | Met        | Cys        | Leu<br>15  | Glu        |
| Lys        | Ile | Gln        | Arg<br>20  | Ala        | Asn        | Glu        | Leu        | Met<br>25  | Gly        | Phe        | Asn        | Asp        | Ser<br>30  | Ser        | Pro        |
| Gly        | Cys | Pro<br>35  | Gly        | Met        | Trp        | Asp        | Asn<br>40  | Ile        | Thr        | Cys        | Trp        | Lys<br>45  | Pro        | Ala        | His        |
| Val<br>50  | Gly | Glu        | Met        | Val        | Leu<br>55  | Val        | Ser        | Cys        | Pro        | Glu        | Leu<br>60  | Phe        | Arg        | Ile        | Phe        |
| Asn<br>65  | Pro | Asp        | Gln        | Val        | Trp<br>70  | Glu        | Thr        | Glu        | Thr        | Ile<br>75  | Gly        | Glu        | Ser        | Asp        | Phe<br>80  |
| Gly        | Asp | Ser        | Asn        | Ser<br>85  | Leu        | Asp        | Leu        | Ser        | Asp<br>90  | Met        | Gly        | Val        | Val        | Ser<br>95  | Arg        |
| Asn        | Cys | Thr        | Glu<br>100 | Asp        | Gly        | Trp        | Ser        | Glu<br>105 | Pro        | Phe        | Pro        | His        | Tyr<br>110 | Phe        | Asp        |
| Ala        | Cys | Gly<br>115 | Phe        | Asp        | Glu        | Tyr        | Glu<br>120 | Ser        | Glu        | Thr        | Gly        | Asp<br>125 | Gln        | Asp        | Tyr        |
| Tyr<br>130 | Tyr | Leu        | Ser        | Val        | Lys        | Ala<br>135 | Leu        | Tyr        | Thr        | Val        | Gly<br>140 | Tyr        | Ser        | Thr        | Ser        |
| Leu<br>145 | Val | Thr        | Leu        | Thr        | Thr<br>150 | Ala        | Met        | Val        | Ile        | Leu<br>155 | Cys        | Arg        | Phe        | Arg        | Lys<br>160 |
| Leu        | His | Cys        | Thr        | Arg<br>165 | Asn        | Phe        | Ile        | His        | Met<br>170 | Asn        | Leu        | Phe        | Val        | Ser<br>175 | Phe        |
| Met        | Leu | Arg        | Ala<br>180 | Ile        | Ser        | Val        | Phe        | Ile<br>185 | Lys        | Asp        | Trp        | Ile        | Leu<br>190 | Tyr        | Ala        |
| Glu        | Gln | Asp<br>195 | Ser        | Asn        | His        | Cys        | Phe<br>200 | Ile        | Ser        | Thr        | Val        | Glu<br>205 | Cys        | Lys        | Ala        |
| Val<br>210 | Met | Val        | Phe        | Phe        | His        | Tyr<br>215 | Cys        | Val        | Val        | Ser        | Asn<br>220 | Tyr        | Phe        | Trp        | Leu        |
| Phe<br>225 | Ile | Glu        | Gly        | Leu        | Tyr<br>230 | Leu        | Phe        | Thr        | Leu        | Leu<br>235 | Val        | Glu        | Thr        | Phe        | Phe<br>240 |
| Pro        | Glu | Arg        | Arg        | Tyr<br>245 | Phe        | Tyr        | Trp        | Tyr        | Thr<br>250 | Ile        | Ile        | Gly        | Trp        | Gly<br>255 | Thr        |
| Pro        | Thr | Val        | Cys<br>260 | Val        | Thr        | Val        | Trp        | Ala<br>265 | Thr        | Leu        | Arg        | Leu        | Tyr<br>270 | Phe        | Asp        |

Asp Thr Gly Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp Val  
275 280 285

Ile Lys Gly Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu Phe  
290 295 300

Ile Gly Ile Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met  
305 310 315 320

Gly Gly Asn Glu Ser Ser Ile Tyr Phe Ser Cys Val Gln Lys Cys Tyr  
325 330 335

Cys Lys Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu  
340 345 350

Ser Thr Ile Thr Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro  
355 360 365

Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val  
370 375 380

Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln  
385 390 395 400

Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln  
405 410 415

Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe  
420 425 430

Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val  
435 440 445

Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile  
450 455 460

Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr  
465 470 475

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

176 -167-

Met Ala Gly Val Val His Val Ser Leu Ala Ala His Cys Gly Ala Cys  
1 5 10 15

Pro Trp Gly Arg Gly Arg Leu Arg Lys Gly Arg Ala Ala Cys Lys Ser  
20 25 30

Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu Leu Ser Val Gly  
35 40 45

Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly Val Val His Val  
50 55 60

Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Pro Ala Met His Ser  
65 70 75 80

Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu Lys Ile Gln  
85 90 95

Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser Pro Gly Cys Pro  
100 105 110

Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala His Val Gly Glu  
115 120 125

Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile Phe Asn Pro Asp  
130 135 140

Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp Phe Gly Asp Ser  
145 150 155 160

Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser Arg Asn Cys Thr  
165 170 175

Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe Asp Ala Cys Gly  
180 185 190

Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr Tyr Tyr Leu  
195 200 205

Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser Leu Val Thr  
210 215 220

Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys Leu His Cys  
225 230 235 240

Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe Met Leu Arg  
245 250 255

Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp  
260 265 270

Ser Asn His Cys Phe Ile Ser Thr Val Glu Cys Lys Ala Val Met Val

176-167-176-167-176-167-

280

Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp Leu Phe Ile Glu  
290 295 300

Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg  
305 310 315 320

Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly Thr Pro Thr Val  
325 330 335

Cys Val Thr Val Trp Ala Thr Leu Arg Leu Tyr Phe Asp Asp Thr Gly  
340 345 350

Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp Val Ile Lys Gly  
355 360 365

Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu Phe Ile Gly Ile  
370 375 380

Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met Gly Gly Asn  
385 390 395 400

Glu Ser Ser Ile Tyr Phe Ser Cys Val Gln Lys Cys Tyr Cys Lys Pro  
405 410 415

Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu Ser Thr Ile  
420 425 430

Thr Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly  
435 440 445

Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys Arg  
450 455 460

Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val  
465 470 475 480

Val Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu Ile  
485 490 495

Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe Ala Val Asp  
500 505 510

Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly Gly  
515 520 525

Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met Ser  
530 535 540

Gly Leu Pro Ala Asp Asn Leu Ala Thr  
545 550

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## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu  
 1 5 10 15  
 Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser Pro  
 20 25 30  
 Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala His  
 35 40 45  
 Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile Phe  
 50 55 60  
 Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp Phe  
 65 70 75 80  
 Gly Asp Ser Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser Arg  
 85 90 95  
 Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe Asp  
 100 105 110  
 Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr  
 115 120 125  
 Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser  
 130 135 140  
 Leu Val Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys  
 145 150 155 160  
 Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe  
 165 170 175  
 Met Leu Arg Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala  
 180 185 190  
 Glu Gln Asp Ser Asn His Cys Phe Ile Ser Thr Val Glu Cys Lys Ala  
 195 200 205

119-170-

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Met | Val | Phe | Phe | His | Tyr | Cys | Val | Val | Ser | Asn | Tyr | Phe | Trp | Leu |
| 210 |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Ile | Glu | Gly | Leu | Tyr | Leu | Phe | Thr | Leu | Leu | Val | Glu | Thr | Phe | Phe |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Pro | Glu | Arg | Arg | Tyr | Phe | Tyr | Trp | Tyr | Thr | Ile | Ile | Gly | Trp | Gly | Thr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Pro | Thr | Val | Cys | Val | Thr | Val | Trp | Ala | Thr | Leu | Arg | Leu | Tyr | Phe | Asp |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asp | Thr | Gly | Cys | Trp | Asp | Met | Asn | Asp | Ser | Thr | Ala | Leu | Trp | Trp | Val |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile | Lys | Gly | Pro | Val | Val | Gly | Ser | Ile | Met | Val | Asn | Phe | Val | Leu | Phe |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ile | Gly | Ile | Ile | Val | Ile | Leu | Val | Gln | Lys | Leu | Gln | Ser | Pro | Asp | Met |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Gly | Gly | Asn | Glu | Ser | Ser | Ile | Tyr | Phe | Cys | Val | Gln | Lys | Cys | Tyr | Cys |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Lys | Pro | Gln | Arg | Ala | Gln | Gln | His | Ser | Cys | Lys | Met | Ser | Glu | Leu | Ser |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Thr | Ile | Thr | Leu | Arg | Leu | Ala | Arg | Ser | Thr | Leu | Leu | Leu | Ile | Pro | Leu |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Phe | Gly | Ile | His | Tyr | Thr | Val | Phe | Ala | Phe | Ser | Pro | Glu | Asn | Val | Ser |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Lys | Arg | Glu | Arg | Leu | Val | Phe | Glu | Leu | Gly | Leu | Gly | Ser | Phe | Gln | Gly |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Phe | Val | Val | Ala | Val | Leu | Tyr | Cys | Phe | Leu | Asn | Gly | Glu | Val | Gln | Ala |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Glu | Ile | Lys | Arg | Lys | Trp | Arg | Ser | Trp | Lys | Val | Asn | Arg | Tyr | Phe | Ala |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Val | Asp | Phe | Lys | His | Arg | His | Pro | Ser | Leu | Ala | Ser | Ser | Gly | Val | Asn |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Gly | Gly | Thr | Gln | Leu | Ser | Ile | Leu | Ser | Lys | Ser | Ser | Ser | Gln | Ile | Arg |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Met | Ser | Gly | Leu | Pro | Ala | Asp | Asn | Leu | Ala | Thr |     |     |     |     |     |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 552 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(B) TYPE: amino acid

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Pro Trp Gly Arg Gly Arg Leu Arg Lys Gly Arg Ala Ala Cys Lys Ser  
20 25 30

Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly Val Val His Val  
50 55 60

Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu Lys Ile Gln  
85 90 95

Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala His Val Gly Glu  
115 120 125

Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp Phe Gly Asp Ser  
145 150 155 160

Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe Asp Ala Cys Gly  
180 185 190 :

Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser Leu Val Thr  
210 215 220



Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys Leu His Cys  
 225 230 235 240  
 Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe Met Leu Arg  
 245 250 255  
 Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp  
 260 265 270  
 Ser Asn His Cys Phe Ile Ser Thr Val Glu Cys Lys Ala Val Met Val  
 275 280 285  
 Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp Leu Phe Ile Glu  
 290 295 300  
 Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg  
 305 310 315 320  
 Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly Thr Pro Thr Val  
 325 330 335  
 Cys Val Thr Val Trp Ala Thr Leu Arg Leu Tyr Phe Asp Asp Thr Gly  
 340 345 350  
 Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp Val Ile Lys Gly  
 355 360 365  
 Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu Phe Ile Gly Ile  
 370 375 380  
 Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met Gly Gly Asn  
 385 390 395 400  
 Glu Ser Ser Ile Tyr Phe Cys Val Gln Lys Cys Tyr Cys Lys Pro Gln  
 405 410 415  
 Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu Ser Thr Ile Thr  
 420 425 430  
 Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile  
 435 440 445  
 His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys Arg Glu  
 450 455 460  
 Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val  
 465 470 475 480  
 Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu Ile Lys  
 485 490 495  
 Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe Ala Val Asp Phe

005574 08204

182-173-

500

505

510

Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly Gly Thr  
515 520 525

Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met Ser Gly  
530 535 540

Leu Pro Ala Asp Asn Leu Ala Thr  
545 550

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 476 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu  
1 5 10 15

Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser Pro  
20 25 30

Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala His  
35 40 45

Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile Phe  
50 55 60

Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp Phe  
65 70 75 80

Gly Asp Ser Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser Arg  
85 90 95

Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe Asp  
100 105 110

Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr  
115 120 125

Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser  
130 135 140

Leu Val Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |
| Leu | His | Cys | Thr | Arg | Asn | Phe | Ile | His | Met | Asn | Leu | Phe | Val | Ser |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |
| Met | Leu | Arg | Ala | Ile | Ser | Val | Phe | Ile | Lys | Asp | Trp | Ile | Leu | Tyr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 | Ala |
| Glu | Gln | Asp | Ser | Asn | His | Cys | Phe | Ile | Ser | Thr | Val | Glu | Cys | Lys |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     | Ala |
| Val | Met | Val | Phe | Phe | His | Tyr | Cys | Val | Val | Ser | Asn | Tyr | Phe | Trp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     | Leu |
| Phe | Ile | Glu | Gly | Leu | Tyr | Leu | Phe | Thr | Leu | Leu | Val | Glu | Thr | Phe |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |
| Pro | Glu | Arg | Arg | Tyr | Phe | Tyr | Trp | Tyr | Thr | Ile | Ile | Gly | Trp | Gly |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |
| Pro | Thr | Val | Cys | Val | Thr | Val | Trp | Ala | Thr | Leu | Arg | Leu | Tyr | Phe |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 | Asp |
| Asp | Thr | Gly | Cys | Trp | Asp | Met | Asn | Asp | Ser | Thr | Ala | Leu | Trp | Trp |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     | Val |
| Ile | Lys | Gly | Pro | Val | Val | Gly | Ser | Ile | Met | Val | Asn | Phe | Val | Leu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     | Phe |
| Ile | Gly | Ile | Ile | Val | Ile | Leu | Val | Gln | Lys | Leu | Gln | Ser | Pro | Asp |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | Met |
| Gly | Gly | Asn | Glu | Ser | Ser | Ile | Tyr | Leu | Thr | Asn | Leu | Ser | Pro | Arg |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |
| Pro | Lys | Lys | Ala | Arg | Glu | Asp | Pro | Leu | Pro | Val | Pro | Ser | Asp | Gln |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 | His |
| Ser | Leu | Pro | Phe | Leu | Arg | Leu | Ala | Arg | Ser | Thr | Leu | Leu | Leu | Ile |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     | Pro |
| Leu | Phe | Gly | Ile | His | Tyr | Thr | Val | Phe | Ala | Phe | Ser | Pro | Glu | Asn |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     | Val |
| Ser | Lys | Arg | Glu | Arg | Leu | Val | Phe | Glu | Leu | Gly | Leu | Gly | Ser | Phe |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     | Gln |
| Gly | Phe | Val | Val | Ala | Val | Leu | Tyr | Cys | Phe | Leu | Asn | Gly | Glu | Val |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |
| Ala | Glu | Ile | Lys | Arg | Lys | Trp | Arg | Ser | Trp | Lys | Val | Asn | Arg | Tyr |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 | Phe |

F03E39T4E5660

Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr  
465 470 475

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 553 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

Met Ala Gly Val Val His Val Ser Leu Ala Ala His Cys Gly Ala Cys  
1 5 10 15

Pro Trp Gly Arg Gly Arg Leu Arg Lys Gly Arg Ala Ala Cys Lys Ser  
20 25 30

Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu Leu Ser Val Gly  
35 40 45

Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly Val Val His Val  
50 55 60

Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Pro Ala Met His Ser  
65 70 75 80

Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu Lys Ile Gln  
85 90 95

Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser Pro Gly Cys Pro  
100 105 110

Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala His Val Gly Glu  
115 120 125

Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile Phe Asn Pro Asp  
130 135 140

Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp Phe Gly Asp Ser  
145 150 155 160

[illegible]

TOE2330.F455650

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ser | Leu | Asp | Leu | Ser | Asp | Met | Gly | Val | Val | Ser | Arg | Asn | Cys | Thr |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Asp | Gly | Trp | Ser | Glu | Pro | Phe | Pro | His | Tyr | Phe | Asp | Ala | Cys | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Phe | Asp | Glu | Tyr | Glu | Ser | Glu | Thr | Gly | Asp | Gln | Asp | Tyr | Tyr | Tyr | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Val | Lys | Ala | Leu | Tyr | Thr | Val | Gly | Tyr | Ser | Thr | Ser | Leu | Val | Thr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Thr | Thr | Ala | Met | Val | Ile | Leu | Cys | Arg | Phe | Arg | Lys | Leu | His | Cys |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Thr | Arg | Asn | Phe | Ile | His | Met | Asn | Leu | Phe | Val | Ser | Phe | Met | Leu | Arg |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ala | Ile | Ser | Val | Phe | Ile | Lys | Asp | Trp | Ile | Leu | Tyr | Ala | Glu | Gln | Asp |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Asn | His | Cys | Phe | Ile | Ser | Thr | Val | Glu | Cys | Lys | Ala | Val | Met | Val |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Phe | Phe | His | Tyr | Cys | Val | Val | Ser | Asn | Tyr | Phe | Trp | Leu | Phe | Ile | Glu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Gly | Leu | Tyr | Leu | Phe | Thr | Leu | Leu | Val | Glu | Thr | Phe | Phe | Pro | Glu | Arg |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Arg | Tyr | Phe | Tyr | Trp | Tyr | Thr | Ile | Ile | Gly | Trp | Gly | Thr | Pro | Thr | Val |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Cys | Val | Thr | Val | Trp | Ala | Thr | Leu | Arg | Leu | Tyr | Phe | Asp | Asp | Thr | Gly |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Cys | Trp | Asp | Met | Asn | Asp | Ser | Thr | Ala | Leu | Trp | Trp | Val | Ile | Lys | Gly |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Pro | Val | Val | Gly | Ser | Ile | Met | Val | Asn | Phe | Val | Leu | Phe | Ile | Gly | Ile |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Ile | Val | Ile | Leu | Val | Gln | Lys | Leu | Gln | Ser | Pro | Asp | Met | Gly | Gly | Asn |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Glu | Ser | Ser | Ile | Tyr | Leu | Thr | Asn | Leu | Ser | Pro | Arg | Val | Pro | Lys | Lys |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Ala | Arg | Glu | Asp | Pro | Leu | Pro | Val | Pro | Ser | Asp | Gln | His | Ser | Leu | Pro |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Phe | Leu | Arg | Leu | Ala | Arg | Ser | Thr | Leu | Leu | Leu | Ile | Pro | Leu | Phe | Gly |

|   |     |     |     |     |
|---|-----|-----|-----|-----|
| 435   |     | 440 |     | 445 |
| Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys Arg |     |     |     |     |
| 450   |     | 455 |     | 460 |
| Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val |     |     |     |     |
| 465   |     | 470 |     | 475 |
| Val Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu Ile |     |     |     |     |
|   | 485 |     | 490 | 495 |
| Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe Ala Val Asp |     |     |     |     |
|   | 500 |     | 505 | 510 |
| Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly Gly |     |     |     |     |
|   | 515 |     | 520 | 525 |
| Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met Ser |     |     |     |     |
|   | 530 |     | 535 | 540 |
| Gly Leu Pro Ala Asp Asn Leu Ala Thr                             |     |     |     |     |
| 545   |     | 550 |     |     |

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..1539

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

|   |     |
|---|-----|
| ATGAGAGGCG GGCGGCACTG GCCCGAGCCG CCTTGCAGGC TGAGAAGCGT CATGGCCAGC | 60  |
| ATCGCGCAGG TCTCCCTGGC TGCTCTCCTC CTGCTGCCTA TGGCCACCGC CATGCATTCC | 120 |
| GACTGCATCT TCAAGAAGGA GCAAGCCATG TGCCTGGAGA AGATCCAGAG GGTGAATGAC | 180 |
| CTGATGGGCT TGAATGACTC CTCCCCAGGG TGCCCTGGGA TGTGGGACAA CATCACGTGT | 240 |
| TGGAAGCCCG CCCACGTGGG TGAGATGGTC CTGGTCAGTT GCCCTGAACT CTTCCGAATC | 300 |
| TTCAACCCAG ACCAAGTCTG GGAGACGGAA ACCATCGGAG AGTTCGGTTT TGCAGACAGT | 360 |

|   |      |
|---|------|
| AAATCCTTGG ATCTCTCAGA CATGAGGGTG GTGAGCCGGA ATTGCACGGA GGATGGATGG   | 420  |
| TCAGAGCCAT TCCCTCATTA TTTCGATGCC TGTGGGTTTG AGGAGTACGA ATCTGAGACT   | 480  |
| GGGGACCAGG ATTACTACTA CCTGTCAGTG AAGGCCCTGT ACACAGTTGG CTACAGCACG   | 540  |
| TCCCTCGTCA CCCTCACCAC TGCCATGGTC ATCCTGTGTC GTTTCCGGAA GCTGCACTGC   | 600  |
| ACCCGCAACT TCATCCACAT GAACCTCTTC GTGTCGTTTA TGCTGAGGGC CATCTCCGTC   | 660  |
| TTCATCAAAG ACTGGATCCT CTATGCTGAG CAGGACAGCA ATCACTGCTT TGTCTCCACT   | 720  |
| GTGGAATGCA AGGCTGTGAT GGTTTTCTTC CACTACTGTG TTGTATCCAA CTACTTCTGG   | 780  |
| CTGTTTCATCG AGGGCCTGTA TCTCTTCACC CTGCTGGTGG AGACCTTCTT CCCCAGAGAGG | 840  |
| AGATAFTTCT ACTGGTACAT CATCATTGGC TGGGGGACAC CAACTGTGTG TGTGTCTGTG   | 900  |
| TGGGCTATGC TGAGGCTCTA CTTCGATGAC ACAGGCTGCT GGGATATGAA TGACAACACG   | 960  |
| GCTCTGTGGT GGGTGATCAA AGGCCCTGTA GTTGGCTCCA TAATGGTTAA TTTTGTGCTC   | 1020 |
| TTTATCGGCA TCATTGTCAT CCTTGTGCAG AAACCTTCAGT CTCCAGACAT GGGAGGCAAC  | 1080 |
| GAGTCCAGCA TCTACTTCAG CTGCGTGCAG AAATGCTACT GCAAGCCACA GCGGGCTCAG   | 1140 |
| CAGCACTCTT GCAAGATGTC AGAACTGTCC ACCATTACTC TACGGCTCGC CAGGTCCACC   | 1200 |
| TTGCTGCTCA TCCCACTCTT TGGAATCCAC TACACTGTCT TTGCTTTCTC CCCGGAGAAC   | 1260 |
| GTGAGCAAGA GGGAGAGACT GGTGTTTGAG CTGGGTCTGG GCTCCTTCCA GGGCTTTGTG   | 1320 |
| GTGGCTGTTT TCTATTGCTT TCTGAATGGA GAGGTGCAGG CGGAGATCAA GAGGAAGTGG   | 1380 |
| CGGAGCTGGA AGGTGAACCG CTACTTCACC ATGGACTTCA AGCACC GGCA CCCATCCCTG  | 1440 |
| GCCAGCAGCG GGGTGAACCG GGGCACCCAG CTCTCCATCC TGAGCAAGAG CAGCTCCCAG   | 1500 |
| ATCCGCATGT CTGGGCTTCC GGCCGACAAC CTGGCCACC                          | 1539 |

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 1..1455

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| ATGAGAGGCG | GGCGGCACTG | GCCCGAGCCG | CCTTGCAGGC | TGAGAAGCGT | CATGGCCAGC | 60   |
| ATCGCGCAGG | TCTCCCTGGC | TGCTCTCCTC | CTGCTGCCTA | TGGCCACCGC | CATGCATTCC | 120  |
| GACTGCATCT | TCAAGAAGGA | GCAAGCCATG | TGCCTGGAGA | AGATCCAGAG | GGTGAATGAC | 180  |
| CTGATGGGCT | TGAATGACTC | CTCCCCAGGG | TGCCCTGGGA | TGTGGGACAA | CATCACGTGT | 240  |
| TGGAAGCCCG | CCCACGTGGG | TGAGATGGTC | CTGGTCAGTT | GCCCTGAACT | CTTCCGAATC | 300  |
| TTCAACCCAG | ACCAAGTCTG | GGAGACGGAA | ACCATCGGAG | AGTTCGGTTT | TGCAGACAGT | 360  |
| AAATCCTTGG | ATCTCTCAGA | CATGAGGGTG | GTGAGCCGGA | ATTGCACGGA | GGATGGATGG | 420  |
| TCAGAGCCAT | TCCCTCATT  | TTTCGATGCC | TGTGGGTTTG | AGGAGTACGA | ATCTGAGACT | 480  |
| GGGACCCAGG | ATTACTACTA | CCTGTCAGTG | AAGGCCCTGT | ACACAGTTGG | CTACAGCACG | 540  |
| TCCTCGTCA  | CCCTCACCAC | TGCCATGGTC | ATCCTGTGTC | GTTTCCGGAA | GCTGCACTGC | 600  |
| ACCGCAACT  | TCATCCACAT | GAACCTCTTC | GTGTCGTTTA | TGCTGAGGGC | CATCTCCGTC | 660  |
| TTGATCAAAG | ACTGGATCCT | CTATGCTGAG | CAGGACAGCA | ATCACTGCTT | TGTCTCCACT | 720  |
| GTGGAATGCA | AGGCTGTGAT | GGTTTTCTTC | CACTACTGTG | TTGTATCCAA | CTACTTCTGG | 780  |
| CTGTTCATCG | AGGGCCTGTA | TCTCTTCACC | CTGCTGGTGG | AGACCTTCTT | CCCCGAGAGG | 840  |
| AGATATTTCT | ACTGGTACAT | CATCATTGGC | TGGGGGACAC | CAACTGTGTG | TGTGTCTGTG | 900  |
| TGGGCTATGC | TGAGGCTCTA | CTTCGATGAC | ACAGGCTGCT | GGGATATGAA | TGACAACACG | 960  |
| GCTCTGTGGT | GGGTGATCAA | AGGCCCTGTA | GTTGGCTCCA | TAATGGTTAA | TTTTGTGCTC | 1020 |
| TTCATCGGCA | TCATTGTCAT | CCTTGTGCAG | AAACTTCAGT | CTCCAGACAT | GGGAGGCAAC | 1080 |
| GAGTCCAGCA | TCTACTTACG | GCTCGCCAGG | TCCACCTTGC | TGCTCATCCC | ACTCTTTGGA | 1140 |
| ATCCACTACA | CTGTCTTTGC | TTTCTCCCCG | GAGAACGTCA | GCAAGAGGGA | GAGACTGGTG | 1200 |
| TTTGAGCTGG | GTCTGGGCTC | CTTCCAGGGC | TTTGTGGTGG | CTGTTCTCTA | TTGCTTTCTG | 1260 |
| AATGGAGAGG | TGCAGGCGGA | GATCAAGAGG | AAGTGGCGGA | GCTGGAAGGT | GAACCGCTAC | 1320 |
| TTCACCATGG | ACTTCAAGCA | CCGGCACCCA | TCCCTGGCCA | GCAGCGGGGT | GAACGGGGGC | 1380 |



ACCCAGCTCT CCATCCTGAG CAAGAGCAGC TCCCAGATCC GCATGTCTGG GCTTCCGGCC 1440  
 GACAACCTGG CCACC 1455

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1401 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..1401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATGCCAGAG TCCTGCAGCT CTCCCTGACT GCTCTCCTGC TGCCTGTGGC TATTGCTATG 60  
 CACTCTGACT GCATCTTCAA GAAGGAGCAA GCCATGTGCC TGGAGAGGAT CCAGAGGGCC 120  
 AAGGACCTGA TGGGACTAAA CGAGTCTTCC CCAGGTTGCC CTGGCATGTG GGACAATATC 180  
 ACATGTTGGA AGCCAGCTCA AGTAGGTGAG ATGGTCCTTG TAAGCTGCCC TGAGGTCTTC 240  
 CGGATCTTCA ACCCGGACCA AGTCTGGATG ACAGAAACCA TAGGAGATTC TGGTTTTGCC 300  
 GATAGTAATT CTTGGAGAT CACAGACATG GGGGTCGTGG GCCGGAAGCTG CACAGAGGAC 360  
 GGCTGGTCGG AGCCCTTCCC CCACTACTTC GATGCTTGTG GGTTTGATGA TTATGAGCCT 420  
 GAGTCTGGAG ATCAGGATTA TTACTACCTG TCGGTGAAGG CTCTCTACAC AGTCGGCTAC 480  
 AGCACTTCCC TCGCCACCCT CACTACTGCC ATGGTCATCT TGTGCCGCTT CCGGAAGCTG 540  
 CATTGCACTC GCAACTTCAT CCACATGAAC CTGTTTGTAT CCTTCATGCT GAGGGCTATC 600  
 TCCGTCTTCA TCAAGGACTG GATCTTGTAC GCCGAGCAGG ACAGCAGTCA CTGCTTCGTT 660  
 TCCACCGTGG AGTGCAAAGC TGTCATGGTT TTCTTCCACT ACTGCGTGGT GTCCAACCTAC 720  
 TTCTGGCTGT TCATTGAAGG CCTGTACCTC TTTACACTGC TGGTGGAGAC CTTCTTCCCT 780  
 GAGAGGAGAT ATTTCTACTG GTACACCATC ATCGGCTGGG GGACACCTAC TGTGTGTGTA 840  
 ACAGTGTGGG CTGTGCTGAG GCTCTATTTT GATGATGCAG GATGCTGGGA TATGAATGAC 900

AGCACAGCTC TGTGGTGGGT GATCAAAGGC CCCGTGGTTG GCTCTATAAT GGTAACTTT 960  
 GTGCTTTTCA TCGGCATCAT CATCATCCTT GTACAGAAGC TGCAGTCCCC AGACATGGGA 1020  
 GGCAACGAGT CCAGCATCTA CTTACGGCTG GCCCCGTCCA CCCTACTGCT CATCCCACTC 1080  
 TTCGGAATCC ACTACACAGT ATTCGCCTTC TCTCCAGAGA ACGTCAGCAA GAGGGAAAGA 1140  
 CTTGTGTTTG AGCTTGGGCT GGGCTCCTTC CAGGGCTTTG TGGTGGCTGT ACTCTACTGC 1200  
 TTCCTGAATG GGGAGGTACA GGCAGAGATT AAGAGGAAAT GGAGGAGCTG GAAGGTGAAC 1260  
 CGTTACTTCA CTATGGACTT CAAGCACCGG CACCCGTCCC TGGCCAGCAG TGGAGTAAAT 1320  
 GGGGGAACCC AGCTGTCCAT CCTGAGCAAG AGCAGCTCCC AGCTCCGCAT GTCCAGCCTC 1380  
 CCGGCCGACA ACTTGGCCAC C 1401

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..1485

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGGCCAGAG TCCTGCAGCT CTCCCTGACT GCTCTCCTGC TGCCTGTGGC TATTGCTATG 60  
 CACTCTGACT GCATCTTCAA GAAGGAGCAA GCCATGTGCC TGGAGAGGAT CCAGAGGGCC 120  
 AACGACCTGA TGGGACTAAA CGAGTCTTCC CCAGGTTGCC CTGGCATGTG GGACAATATC 180  
 ACATGTTGGA AGCCAGCTCA AGTAGGTGAG ATGGTCCTTG TAAGCTGCCC TGAGGTCTTC 240  
 CGGATCTTCA ACCCGGACCA AGTCTGGATG ACAGAAACCA TAGGAGATTC TGGTTTTGCC 300  
 GATAGTAATT CCTTGGAGAT CACAGACATG GGGGTCGTGG GCCGGAAGTG CACAGAGGAC 360  
 GGCTGGTCGG AGCCCTTCCC CCACTACTTC GATGCTTGTG GGTTTGATGA TTATGAGCCT 420  
 GAGTCTGGAG ATCAGGATTA TTACTACCTG TCGGTGAAGG CTCTCTACAC AGTCGGCTAC 480

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| AGCACTTCCC | TCGCCACCCT | CACTACTGCC | ATGGTCATCT | TGTGCCGCTT | CCGGAAGCTG | 540  |
| CATTGCACTC | GCAACTTCAT | CCACATGAAC | CTGTTTGTAT | CCTTCATGCT | GAGGGCTATC | 600  |
| TCCGTCTTCA | TCAAGGACTG | GATCTTGTA  | GCCGAGCAGG | ACAGCAGTCA | CTGCTTCGTT | 660  |
| TCCACCGTGG | AGTGCAAAGC | TGTCATGGTT | TTCTTCCACT | ACTGCGTGGT | GTCCAACTAC | 720  |
| TTCTGGCTGT | TCATTGAAGG | CCTGTACCTC | TTTACACTGC | TGGTGGAGAC | CTTCTTCCCT | 780  |
| GAGAGGAGAT | ATTTCTACTG | GTACACCATC | ATCGGCTGGG | GGACACCTAC | TGTGTGTGTA | 840  |
| ACAGTGTGGG | CTGTGCTGAG | GCTCTATTTT | GATGATGCAG | GATGCTGGGA | TATGAATGAC | 900  |
| AGCACAGCTC | TGTGGTGGGT | GATCAAAGGC | CCCGTGTTG  | GCTCTATAAT | GGTAACTTT  | 960  |
| GTGCTTTTCA | TCGGCATCAT | CATCATCCTT | GTACAGAAGC | TGCAGTCCCC | AGACATGGGA | 1020 |
| GGCAACGAGT | CCAGCATCTA | CTTCAGCTGC | GTGCAGAAAT | GCTACTGCAA | GCCACAGCGG | 1080 |
| GCTCAGCAGC | ACTCTTGCAA | GATGTCAGAA | CTATCCACCA | TTACTCTACG | GCTGGCCCCG | 1140 |
| TCCACCCTAC | TGCTCATCCC | ACTCTTCGGA | ATCCACTACA | CAGTATTTCG | CTTCTCTCCA | 1200 |
| GAGAACGTCA | GCAAGAGGGA | AAGACTTGTG | TTTGAGCTTG | GGCTGGGCTC | CTTCCAGGGC | 1260 |
| TTTGTGGTGG | CTGTACTCTA | CTGCTTCCTG | AATGGGGAGG | TACAGGCAGA | GATTAAGAGG | 1320 |
| AAATGGAGGA | GCTGGAAGGT | GAACCGTTAC | TTCACTATGG | ACTTCAAGCA | CCGGCACCCG | 1380 |
| TCCCTGGCCA | GCAGTGGAGT | AAATGGGGGA | ACCCAGCTGT | CCATCCTGAG | CAAGAGCAGC | 1440 |
| TCCCAGCTCC | GCATGTCCAG | CCTCCCGGCC | GACAACTTGG | CCACC      |            | 1485 |

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1575 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..1575

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

|             |            |             |            |            |            |      |
|-------------|------------|-------------|------------|------------|------------|------|
| ATGGCTGGTG  | TCGTGCACGT | TTCCCTGGCT  | GCTCACTGCG | GGGCCTGTCC | GTGGGGCCGG | 60   |
| GGCAGACTCC  | GCAAAGGACG | CGCAGCCTGC  | AAGTCCGCGG | CCCAGAGACA | CATTGGGGCT | 120  |
| GACCTGCCGC  | TGCTGTCAGT | GGGAGGCCAG  | TGGTGCTGGC | CAAGAAGTGT | CATGGCTGGT | 180  |
| GTCGTGCACG  | TTTCCCTGGC | TGCTCTCCTC  | CTGCTGCCTA | TGGCCCCTGC | CATGCATTCT | 240  |
| GACTGCATCT  | TCAAGAAGGA | GCAAGCCATG  | TGCCTGGAGA | AGATCCAGAG | GGCCAATGAG | 300  |
| CTGATGGGCT  | TCAATGATTG | CTCTCCAGGC  | TGTCCTGGGA | TGTGGGACAA | CATCACGTGT | 360  |
| TGGAAGCCCG  | CCCATGTGGG | TGAGATGGTC  | CTGGTCAGCT | GCCCTGAGCT | CTTCCGAATC | 420  |
| TTCAACCCAG  | ACCAAGTCTG | GGAGACCGAA  | ACCATTGGAG | AGTCTGATTT | TGGTGACAGT | 480  |
| AACTCCTTAG  | ATCTCTCAGA | CATGGGAGTG  | GTGAGCCGGA | ACTGCACGGA | GGATGGCTGG | 540  |
| TCGGAACCCT  | TCCCTCATTG | CTTTGATGCC  | TGTGGGTTTG | ATGAATATGA | ATCTGAGACT | 600  |
| GGGGACCAGG  | ATTATTACTA | CCTGTCAGTG  | AAGGCCCTCT | ACACGGTTGG | CTACAGCACA | 660  |
| TGCTCTCGTCA | CCCTCACCAC | TGCCATGGTC  | ATCCTTTGTC | GCTTCCGGAA | GCTGCACTGC | 720  |
| ACACGCAACT  | TCATCCACAT | GAACCTGTTT  | GTGTCGTTCA | TGCTGAGGGC | GATCTCCGTC | 780  |
| TTTATCAAAG  | ACTGGATTCT | GTATGCGGAG  | CAGGACAGCA | ACCACTGCTT | CATCTCCACT | 840  |
| GTGGAATGTA  | AGGCCGTCAT | GGTTTTCTTC  | CACTACTGTG | TTGTGTCCAA | CTACTTCTGG | 900  |
| CTGTTCATCG  | AGGGCCTGTA | CCTCTTCACT  | CTGCTGGTGG | AGACCTTCTT | CCCTGAAAGG | 960  |
| AGATACTTCT  | ACTGGTACAC | CATCATTTGGC | TGGGGGTCCC | CAACTGTGTG | TGTGACAGTG | 1020 |
| TGGGCTACGC  | TGAGACTCTA | CTTTGATGAC  | ACAGGCTGCT | GGGATATGAA | TGACAGCACA | 1080 |
| GCTCTGTGGT  | GGGTGATCAA | AGGCCCTGTG  | GTTGGCTCTA | TCATGGTTAA | CTTTGTGCTT | 1140 |
| TTTATTGGCA  | TTATCGTCAT | CCTTGTGCAG  | AAACTTCAGT | CTCCAGACAT | GGGAGGCAAT | 1200 |
| GAGTCCAGCA  | TCTACTTGCG | ACTGGCCCGG  | TCCACCCTGC | TGCTCATCCC | ACTATTCGGA | 1260 |
| ATCCACTACA  | CAGTATTTGC | CTTCTCCCCA  | GAGAATGTCA | GCAAAAGGGA | AAGACTCGTG | 1320 |
| TTTGAGCTGG  | GGCTGGGCTC | CTTCCAGGGC  | TTTGTGGTGG | CTGTTCTCTA | CTGTTTTCTG | 1380 |
| AATGGTGAGG  | TACAAGCGGA | GATCAAGCGA  | AAATGGCGAA | GCTGGAAGGT | GAACCGTTAC | 1440 |
| TTCGCTGTGG  | ACTTCAAGCA | CCGACACCCG  | TCTCTGGCCA | GCAGTGGGGT | GAATGGGGGC | 1500 |
| ACCCAGCTCT  | CCATCCTGAG | CAAGAGCAGC  | TCCCAAATCC | GCATGTCTGG | CCTCCCTGCT | 1560 |

GACAATCTGG CCACC

1575

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1659 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..1659

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

|  |     |
|--|-----|
| ATGGCTGGTG TCGTGCACGT TTCCCTGGCT GCTCACTGCG GGGCCTGTCC GTGGGGCCGG  | 60  |
| GGCAGACTCC GCAAAGGACG CGCAGCCTGC AAGTCCGCGG CCCAGAGACA CATTTGGGGCT | 120 |
| GAGCTGCCGC TGCTGTCAGT GGGAGGCCAG TGGTGCTGGC CAAGAAGTGT CATGGCTGGT  | 180 |
| GTGGTGACAG TTTCCCTGGC TGCTCTCCTC CTGCTGCCTA TGGCCCCTGC CATGCATTCT  | 240 |
| GAGTGCATCT TCAAGAAGGA GCAAGCCATG TGCCTGGAGA AGATCCAGAG GGCCAATGAG  | 300 |
| CTGATGGGCT TCAATGATTC CTCTCCAGGC TGTCCTGGGA TGTGGGACAA CATCACGTGT  | 360 |
| TGGAAGCCCG CCCATGTGGG TGAGATGGTC CTGGTCAGCT GCCCTGAGCT CTTCCGAATC  | 420 |
| TTCAACCCAG ACCAAGTCTG GGAGACCGAA ACCATTGGAG AGTCTGATTT TGGTGACAGT  | 480 |
| AACTCCTTAG ATCTCTCAGA CATGGGAGTG GTGAGCCGGA ACTGCACGGA GGATGGCTGG  | 540 |
| TCGGAACCCT TCCCTCATTG CTTTGATGCC TGTGGGTTTG ATGAATATGA ATCTGAGACT  | 600 |
| GGGGACCAGG ATTATTACTA CCTGTCAGTG AAGGCCCTCT ACACGGTTGG CTACAGCACA  | 660 |
| TCCCTCGTCA CCCTCACCAC TGCCATGGTC ATCCTTTGTC GCTTCCGGAA GCTGCACTGC  | 720 |
| ACACGCAACT TCATCCACAT GAACCTGTTT GTGTCGTTCA TGCTGAGGGC GATCTCCGTC  | 780 |
| TTCATCAAAG ACTGGATTCT GTATGCGGAG CAGGACAGCA ACCACTGCTT CATCTCCACT  | 840 |
| GTGGAATGTA AGGCCGTCAT GGTTCCTTTC CACTACTGTG TTGTGTCCAA CTACTTCTGG  | 900 |
| CTGTTTCATCG AGGGCCTGTA CCTCTTCACT CTGCTGGTGG AGACCTTCTT CCCTGAAAGG | 960 |

AGATACTTCT ACTGGTACAC CATCATTGGC TGGGGGACCC CAACTGTGTG TGTGACAGTG 1020  
 TGGGCTACGC TGAGACTCTA CTTTGATGAC ACAGGCTGCT GGGATATGAA TGACAGCACA 1080  
 GCTCTGTGGT GGGTGATCAA AGGCCCTGTG GTTGGCTCTA TCATGGTTAA CTTTGTGCTT 1140  
 TTTATTGGCA TTATCGTCAT CCTTGTCAG AAACCTCAGT CTCCAGACAT GGGAGGCAAT 1200  
 GAGTCCAGCA TCTACTTCAG CTGCGTGCAG AAATGCTACT GCAAGCCACA GCGGGCTCAG 1260  
 CAGCACTCTT GCAAGATGTC AGAACTGTCC ACCATTACTC TGCGACTGGC CCGGTCCACC 1320  
 CTGCTGCTCA TCCCACTATT CGGAATCCAC TACACAGTAT TTGCCTTCTC CCCAGAGAAT 1380  
 GTCAGCAAAA GGGAAAGACT CGTGTTTGAG CTGGGGCTGG GCTCCTTCCA GGGCTTTGTG 1440  
 GTGGCTGTTT TCTACTGTTT TCTGAATGGT GAGGTACAAG CGGAGATCAA GCGAAAATGG 1500  
 CGAAGCTGGA AGGTGAACCG TTA CTTCGCT GTGGACTTCA AGCACCGACA CCCGTCTCTG 1560  
 GCCAGCAGTG GGGTGAATGG GGGCACCCAG CTCTCCATCC TGAGCAAGAG CAGCTCCCAA 1620  
 ATCCGCATGT CTGGCCTCCC TGCTGACAAT CTGGCCACC 1659

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1656 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..1656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ATGGCTGGTG TCGTGACAGT TTCCCTGGCT GCTCACTGCG GGGCCTGTCC GTGGGGCCGG 60  
 GGCAGACTCC GCAAAGGACG CGCAGCCTGC AAGTCCGCGG CCCAGAGACA CATTGGGGCT 120  
 GACCTGCCGC TGCTGTCAGT GGGAGGCCAG TGGTGCTGGC CAAGAAGTGT CATGGCTGGT 180  
 GTCGTGCACG TTTCCCTGGC TGCTCTCCTC CTGCTGCCTA TGGCCCCTGC CATGCATTCT 240  
 GACTGCATCT TCAAGAAGGA GCAAGCCATG TGCCTGGAGA AGATCCAGAG GGCCAATGAG 300

|  |      |
|--|------|
| CTGATGGGCT TCAATGATTC CTCTCCAGGC TGTCTGGGA TGTGGGACAA CATCACGTGT   | 360  |
| TGGAAGCCCG CCCATGTGGG TGAGATGGTC CTGGTCAGCT GCCCTGAGCT CTTCCGAATC  | 420  |
| TTCAACCCAG ACCAAGTCTG GGAGACCGAA ACCATTGGAG AGTCTGATTT TGGTGACAGT  | 480  |
| AACTCCTTAG ATCTCTCAGA CATGGGAGTG GTGAGCCGGA ACTGCACGGA GGATGGCTGG  | 540  |
| TCGGAACCCT TCCCTCATTA CTTTGATGCC TGTGGGTTTG ATGAATATGA ATCTGAGACT  | 600  |
| GGGGACCAGG ATTATTACTA CCTGTCAGTG AAGGCCCTCT ACACGGTTGG CTACAGCACA  | 660  |
| TCCCTCGTCA CCCTCACCAC TGCCATGGTC ATCCTTTGTC GCTTCCGGAA GCTGCACTGC  | 720  |
| ACACGCAACT TCATCCACAT GAACCTGTTT GTGTCGTTCA TGCTGAGGGC GATCTCCGTC  | 780  |
| TTCAATCAAAG ACTGGATTCT GTATGCGGAG CAGGACAGCA ACCACTGCTT CATCTCCACT | 840  |
| GTGGAATGTA AGGCCGTCAT GGTTTTCTTC CACTACTGTG TTGTGTCCAA CTACTTCTGG  | 900  |
| CTGTTTCATCG AGGGCCTGTA CCTCTTCACT CTGCTGGTGG AGACCTTCTT CCCTGAAAGG | 960  |
| AGATACTTCT ACTGGTACAC CATCATTTGGC TGGGGGACCC CAACTGTGTG TGTGACAGTG | 1020 |
| TGGGCTACGC TGAGACTCTA CTTTGATGAC ACAGGCTGCT GGGATATGAA TGACAGCACA  | 1080 |
| GCTGTGTGGT GGGTGATCAA AGGCCCTGTG GTTGGCTCTA TCATGGTTAA CTTTGTGCTT  | 1140 |
| TTTATTGGCA TTATCGTCAT CCTTGTGCAG AAACCTCAGT CTCCAGACAT GGGAGGCAAT  | 1200 |
| GAGTCCAGCA TCTACTTCTG CGTGCAGAAA TGCTACTGCA AGCCACAGCG GGCTCAGCAG  | 1260 |
| CACTCTTGCA AGATGTCAGA ACTGTCCACC ATTACTCTGC GACTGGCCCG GTCCACCCTG  | 1320 |
| CTGCTCATCC CACTATTCTG AATCCACTAC ACAGTATTTG CCTTCTCCCC AGAGAATGTC  | 1380 |
| AGCAAAAGGG AAAGACTCGT GTTTGAGCTG GGGCTGGGCT CCTTCCAGGG CTTTGTGGTG  | 1440 |
| GCTGTTCTCT ACTGTTTTCT GAATGGTGAG GTACAAGCGG AGATCAAGCG AAAATGGCGA  | 1500 |
| AGCTGGAAGG TGAACCGTTA CTTGCTGTG GACTTCAAGC ACCGACACCC GTCTCTGGCC   | 1560 |
| AGCAGTGGGG TGAATGGGGG CACCCAGCTC TCCATCCTGA GCAAGAGCAG CTCCCAAATC  | 1620 |
| CGCATGTCTG GCCTCCCTGC TGACAATCTG GCCACC                            | 1656 |

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1659 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 1..1659

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

|  |      |
|--|------|
| ATGGCTGGTG TCGTGACAGT TTCCCTGGCT GCTCACTGCG GGGCCTGTCC GTGGGGCCGG  | 60   |
| GGCAGACTCC GCAAAGGACG CGCAGCCTGC AAGTCCGCGG CCCAGAGACA CATTGGGGCT  | 120  |
| GACCTGCCGC TGCTGTCAGT GGGAGGCCAG TGGTGCTGGC CAAGAAGTGT CATGGCTGGT  | 180  |
| GTGGTGCACG TTTCCCTGGC TGCTCTCCTC CTGCTGCCTA TGGCCCCTGC CATGCATTCT  | 240  |
| GACGTGCATCT TCAAGAAGGA GCAAGCCATG TGCCTGGAGA AGATCCAGAG GGCCAATGAG | 300  |
| CTGATGGGCT TCAATGATTC CTCTCCAGGC TGTCTGGGA TGTGGGACAA CATCACGTGT   | 360  |
| TGGAAGCCCG CCCATGTGGG TGAGATGGTC CTGGTCAGCT GCCCTGAGCT CTTCCGAATC  | 420  |
| TTCAACCCAG ACCAAGTCTG GGAGACCGAA ACCATTGGAG AGTCTGATTT TGGTGACAGT  | 480  |
| AACTCCTTAG ATCTCTCAGA CATGGGAGTG GTGAGCCGGA ACTGCACGGA GGATGGCTGG  | 540  |
| TGGGAACCCT TCCCTCATTA CTTTGATGCC TGTGGGTTTG ATGAATATGA ATCTGAGACT  | 600  |
| GGGGACCAGG ATTATTACTA CCTGTCAGTG AAGGCCCTCT ACACGGTTGG CTACAGCACA  | 660  |
| TCCCTCGTCA CCCTCACCAC TGCCATGGTC ATCCTTTGTC GCTTCCGGAA GCTGCACTGC  | 720  |
| ACACGCAACT TCATCCACAT GAACCTGTTT GTGTCGTTCA TGCTGAGGGC GATCTCCGTC  | 780  |
| TTCATCAAAG ACTGGATTCT GTATGCGGAG CAGGACAGCA ACCACTGCTT CATCTCCACT  | 840  |
| GTGGAATGTA AGGCCGTCAT GGTTTCTTC CACTACTGTG TTGTGTCCAA CTACTTCTGG   | 900  |
| CTGTTCATCG AGGGCCTGTA CCTCTTCACT CTGCTGGTGG AGACCTTCTT CCCTGAAAGG  | 960  |
| AGATACTTCT ACTGGTACAC CATCATTTGGC TGGGGGACCC CAACTGTGTG TGTGACAGTG | 1020 |
| TGGGCTACGC TGAGACTCTA CTTTGATGAC ACAGGCTGCT GGGATATGAA TGACAGCACA  | 1080 |
| GCTCTGTGGT GGGTGATCAA AGGCCCTGTG GTTGGCTCTA TCATGGTTAA CTTTGTGCTT  | 1140 |
| TTTATTGGCA TTATCGTCAT CCTTGTGCAG AACTTCAGT CTCCAGACAT GGGAGGCAAT   | 1200 |



|  |      |
|--|------|
| GAGTCCAGCA TCTACTTAAC AAATTTAAGC CCGCGAGTCC CCAAGAAAGC CCGAGAGGAC  | 1260 |
| CCCCTGCCTG TGCCCTCAGA CCAGCATTC A CTCCCTTTCC TCGGACTGGC CCGGTCCACC | 1320 |
| CTGCTGCTCA TCCCCTATT CGGAATCCAC TACACAGTAT TTGCCTTCTC CCCAGAGAAT   | 1380 |
| GTCAGCAAAA GGGAAAGACT CGTGTTTGAG CTGGGGCTGG GCTCCTTCCA GGGCTTTGTG  | 1440 |
| GTGGCTGTTC TCTACTGTTT TCTGAATGGT GAGGTACAAG CGGAGATCAA GCGAAAATGG  | 1500 |
| CGAAGCTGGA AGGTGAACCG TTA CTTCGCT GTGGACTTCA AGCACCGACA CCCGTCTCTG | 1560 |
| GCCAGCAGTG GGGTGAATGG GGGCACCCAG CTCTCCATCC TGAGCAAGAG CAGCTCCCAA  | 1620 |
| ATCCGCATGT CTGGCCTCCC TGCTGACAAT CTGGCCACC                         | 1659 |

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 498..2036

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

|   |     |
|---|-----|
| TGGCCTGCAC CCCACCCCCC AGCCTGCGAA GACGGGGGGA GGCGGTGGTC GGTCGCCTCC | 60  |
| CTCCTGCCCC CGGCCTGGCT TCGCGGTGGA GGCGGTGCCT CTCCGGCAAG GCAGACCAGG | 120 |
| CTGGGCGGAC GCGCGGCGCG GGGCGGGCTA GGGAAGGCCG GGGGCCTCGC GCTCGGGCCC | 180 |
| CGGGCGGCGA CTGACAGCGG CGGCGGCGGC GGCAGCGGCT CCAAGGCGAG CGTGGTCCCC | 240 |
| GCGTGCGCAC AAGCTCGCCG CCGCGCAGGG ACCCACGGAC ACCGGCGCCG GGCGGACACA | 300 |
| CAGACGCGGA GATCGGGCTC TACGCGCGCT ACTCAGCGCA CGAGCTCCCC ATCCCTGGGC | 360 |
| GGAGCGGGGC GCGGACTCGC CGCTGCGCGC CCTCCCCGCG GAGTCTGCCC CGGGCAGACC | 420 |
| CGCAGCCCGC GGCCCCGCCG CGAGGCCCTT GGGTGAGCAG CCTGTAGACA CCTGGGGTTG | 480 |
| AGCAGTGGCG GCTGTGAATG AGAGGCGGGC GGCCTGGCC CGAGCCGCCT TGCAGGCTGA  | 540 |

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| GAAGCGTCAT | GGCCAGCATC | GCGCAGGTCT | CCCTGGCTGC | TCTCCTCCTG | CTGCCTATGG | 600  |
| CCACCGCCAT | GCATTCCGAC | TGCATCTTCA | AGAAGGAGCA | AGCCATGTGC | CTGGAGAAGA | 660  |
| TCCAGAGGGT | GAATGACCTG | ATGGGCTTGA | ATGACTCCTC | CCCAGGGTGC | CCTGGGATGT | 720  |
| GGGACAACAT | CACGTGTTGG | AAGCCCGCCC | ACGTGGGTGA | GATGGTCCTG | GTCAGTTGCC | 780  |
| CTGAACTCTT | CCGAATCTTC | AACCCAGACC | AAGTCTGGGA | GACGGAAACC | ATCGGAGAGT | 840  |
| TCGGTTTTGC | AGACAGTAAA | TCCTTGGATC | TCTCAGACAT | GAGGGTGGTG | AGCCGGAATT | 900  |
| GCACGGAGGA | TGGATGGTCA | GAGCCATTCC | CTCATTATTT | CGATGCCTGT | GGGTTTGAGG | 960  |
| AGTACGAATC | TGAGACTGGG | GACCAGGATT | ACTACTACCT | GTCAGTGAAG | GCCCTGTACA | 1020 |
| CAGTTGGCTA | CAGCACGTCC | CTCGTCACCC | TCACCACTGC | CATGGTCATC | CTGTGTCGTT | 1080 |
| TCCGGAAGCT | GCACTGCACC | CGCAACTTCA | TCCACATGAA | CCTCTTCGTG | TCGTTTATGC | 1140 |
| TGAGGGCCAT | CTCCGTCTTC | ATCAAAGACT | GGATCCTCTA | TGCTGAGCAG | GACAGCAATC | 1200 |
| ACTGCTTTGT | CTCCACTGTG | GAATGCAAGG | CTGTGATGGT | TTTCTTCCAC | TACTGTGTTG | 1260 |
| TATCCAATA  | CTTCTGGCTG | TTCATCGAGG | GCCTGTATCT | CTTCACCCTG | CTGGTGGAGA | 1320 |
| CCTTCTTCCC | CGAGAGGAGA | TATTTCTACT | GGTACATCAT | CATTGGCTGG | GGGACACCAA | 1380 |
| CTGTGTGTGT | GTCTGTGTGG | GCTATGCTGA | GGCTCTACTT | CGATGACACA | GGCTGCTGGG | 1440 |
| ATATGAATGA | CAACACGGCT | CTGTGGTGGG | TGATCAAAGG | CCCTGTAGTT | GGCTCCATAA | 1500 |
| TGGTTAATTT | TGTGCTCTTC | ATCGGCATCA | TTGTCATCCT | TGTGCAGAAA | CTTCAGTCTC | 1560 |
| CAGACATGGG | AGGCAACGAG | TCCAGCATCT | ACTTCAGCTG | CGTGCAGAAA | TGCTACTGCA | 1620 |
| AGCCACAGCG | GGCTCAGCAG | CACTCTTGCA | AGATGTCAGA | ACTGTCCACC | ATTACTCTAC | 1680 |
| GGCTCGCCAG | GTCCACCTTG | CTGCTCATCC | CACTCTTTGG | AATCCACTAC | ACTGTCTTTG | 1740 |
| CTTTCTCCCC | GGAGAACGTC | AGCAAGAGGG | AGAGACTGGT | GTTTGAGCTG | GGTCTGGGCT | 1800 |
| CCTTCCAGGG | CTTTGTGGTG | GCTGTTCTCT | ATTGCTTTCT | GAATGGAGAG | GTGCAGGCGG | 1860 |
| AGATCAAGAG | GAAGTGGCGG | AGCTGGAAGG | TGAACCGCTA | CTTCACCATG | GACTTCAAGC | 1920 |
| ACCGGCACCC | ATCCCTGGCC | AGCAGCGGGG | TGAACGGGGG | CACCCAGCTC | TCCATCCTGA | 1980 |
| GCAAGAGCAG | CTCCCAGATC | CGCATGTCTG | GGCTTCCGGC | CGACAACCTG | GCCACCTGAG | 2040 |
| CCCACCCTGC | CCCCTCCTCT | CCTCTGTACG | CAGGCTGGGG | CTGTGGTGGG | GCGCCGGCCC | 2100 |

|   |      |
|---|------|
| ACGCATGTTG TGCCTCTTCT CGCCTTCGGG CAGGCCCCGG GCTGGGCGCC TGGCCCCCGA   | 2160 |
| GGTTGGAGAA GGATGCGGGA CAGGCAGCTG TTTAGCCTTC CTGTTTTTGGC GCTGGCCCCAA | 2220 |
| CCACCGTGGG TCCCTGGGCC TGCACCCAGA CATGTAATAC TCCTTAATTG GGAAGTCATC   | 2280 |
| CATTCTTTCC CTTTCCCAAG TCCTTGCTTA TTAAGAGGTT CAAGTCACCT ACCCAATTCA   | 2340 |
| GAAGCTTAAG TAACCACTAA CCACCGTGAC TGCCTGGGAG GCCTCCCATG GGCTGAGCTA   | 2400 |
| CTGACTTGGC TTTGGGGGCC TTGGGCTGGG GCCCTCCTTA AAGCCCCCCC TGAAATTGTC   | 2460 |
| GGACCTCAA GTGTGACTCC TTTGAGTCTA CTCGCCACCC CCGTGGCCCT TTGCAGCCCT    | 2520 |
| GGTCCAGTCA CCGAGGTTAC TGGAAGTCCA GCTTGGATGG CCAGACAGCT TTTTGGCACA   | 2580 |
| GGGAGACCCA TGCTCACCCA ACATTTTAGT GTCCAGGTGC CCAGGTGCCC AGGTGCCCAG   | 2640 |
| CTCCTGGGCA TCAGACAGTG GGAAAGCTCC AGGGATCTAC CATTCAGAGA CTTCAGTTTG   | 2700 |
| GATGTAGGGC TAAGGCCAGA GAAAAGTTCT GGAGCTTTTC ATTTGGCCCA AGAAAAAACT   | 2760 |
| GCCAAGATCC AGAAAAGTGG ATCTGAGTGG AATTAGATG CAAAGAGCTT GGAG          | 2814 |

## (2) INFORMATION FOR SEQ ID NO:39:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2730 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 498..1952

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

|   |     |
|---|-----|
| TGGCCTGCAC CCCACCCCCC AGCCTGCGAA GACGGGGGGA GGCGGTGGTC GGTGCGCTCC | 60  |
| CTCCTGCCCC CGGCCTGGCT TCGCGGTGGA GGCGGTGCCT CTCCGGCAAG GCAGACCAGG | 120 |
| CTGGGCGGAC GCGCGGCGCG GGGCGGGCTA GGGAAGGCCG GGGGCCTCGC GCTCGGGCCC | 180 |
| CGGGCGGCGA CTGACAGCGG CGGCGGCGGC GGCAGCGGCT CCAAGGCGAG CGTGGTCCCC | 240 |
| GCGTGCGCAC AAGCTCGCCG CCGCGCAGGG ACCCACGGAC ACCGGCGCCG GGCGGACACA | 300 |

|  |      |
|--|------|
| CAGACGCGGA GATCGGGCTC TACGCGCGCT ACTCAGCGCA CGAGCTCCCC ATCCCTGGGC  | 360  |
| GGAGCGGGGC GCGGACTCGC CGCTGCGCGC CCTCCCCGCG GAGTCTGCCC CGGGCAGACC  | 420  |
| CGCAGCCCCG GGGCCCGCCG CGAGGCCCCCT GGGTGAGCAG CCTGTAGACA CCTGGGGTTG | 480  |
| AGCAGTGGCG GCTGTGAATG AGAGGCGGGC GGCAGTGGCC CGAGCCGCCT TGCAGGCTGA  | 540  |
| GAAGCGTCAT GGCCAGCATC GCGCAGGTCT CCCTGGCTGC TCTCCTCCTG CTGCCTATGG  | 600  |
| CCACCGCCAT GCATTCCGAC TGCATCTTCA AGAAGGAGCA AGCCATGTGC CTGGAGAAGA  | 660  |
| TCCAGAGGGT GAATGACCTG ATGGGCTTGA ATGACTCCTC CCCAGGGTGC CCTGGGATGT  | 720  |
| GGGACAACAT CACGTGTTGG AAGCCCGCCC ACGTGGGTGA GATGGTCCTG GTCAGTTGCC  | 780  |
| CTGAACTCTT CCGAATCTTC AACCAGACC AAGTCTGGGA GACGGAAACC ATCGGAGAGT   | 840  |
| TCCGTTTTGC AGACAGTAAA TCCTTGGATC TCTCAGACAT GAGGGTGGTG AGCCGGAATT  | 900  |
| GCACGGAGGA TGGATGGTCA GAGCCATTCC CTCATTATTT CGATGCCTGT GGGTTTGAGG  | 960  |
| AGTACGAATC TGAGACTGGG GACCAGGATT ACTACTACCT GTCAGTGAAG GCCCTGTACA  | 1020 |
| CAGTTGGCTA CAGCACGTCC CTCGTCACCC TCACCACTGC CATGGTCATC CTGTGTCTGT  | 1080 |
| TCCGGAAGCT GCACTGCACC CGCAACTTCA TCCACATGAA CCTCTTCGTG TCGTTTATGC  | 1140 |
| TGAGGGCCAT CTCCGTCTTC ATCAAAGACT GGATCCTCTA TGCTGAGCAG GACAGCAATC  | 1200 |
| ACTGCTTTGT CTCCACTGTG GAATGCAAGG CTGTGATGGT TTTCTTCCAC TACTGTGTTG  | 1260 |
| TATCCAATA CTTCTGGCTG TTCATCGAGG GCCTGTATCT CTTACCCTG CTGGTGGAGA    | 1320 |
| CCTTCTTCCC CGAGAGGAGA TATTTCTACT GGTACATCAT CATTGGCTGG GGGACACCAA  | 1380 |
| CTGTGTGTGT GTCTGTGTGG GCTATGCTGA GGCTCTACTT CGATGACACA GGCTGCTGGG  | 1440 |
| ATATGAATGA CAACACGGCT CTGTGGTGGG TGATCAAAGG CCCTGTAGTT GGCTCCATAA  | 1500 |
| TGGTTAATTT TGTGCTCTTC ATCGGCATCA TTGTCATCCT TGTGCAGAAA CTTAGTCTC   | 1560 |
| CAGACATGGG AGGCAACGAG TCCAGCATCT ACTTACGGCT CGCCAGGTCC ACCTTGCTGC  | 1620 |
| TCATCCCACT CTTTGAATC CACTACACTG TCTTTGCTTT CTCCCCGAG AACGTCAGCA    | 1680 |
| AGAGGGAGAG ACTGGTGTTT GAGCTGGGTC TGGGCTCCTT CCAGGGCTTT GTGGTGGCTG  | 1740 |
| TTCTCTATTG CTTTCTGAAT GGAGAGGTGC AGGCGGAGAT CAAGAGGAAG TGGCGGAGCT  | 1800 |
| GGAAGGTGAA CCGCTACTTC ACCATGGACT TCAAGCACCG GCACCCATCC CTGGCCAGCA  | 1860 |

|   |      |
|---|------|
| GCGGGGTGAA CCGGGGCACC CAGCTCTCCA TCCTGAGCAA GAGCAGCTCC CAGATCCGCA | 1920 |
| TGTCTGGGCT TCCGGCCGAC AACCTGGCCA CCTGAGCCCA CCCTGCCCCC TCCTCTCCTC | 1980 |
| TGTACGCAGG CTGGGGCTGT GGTGGGGCGC CGGCCACGC ATGTTGTGCC TCTTCTCGCC  | 2040 |
| TTCGGGCAGG CCCC GGCTG GCGCCTGGC CCCC GAGGTT GGAGAAGGAT GCGGGACAGG | 2100 |
| CAGCTGTTTA GCCTTCCTGT TTTGGCGCTG GCCCAACCAC CGTGGGTCCC TGGGCCTGCA | 2160 |
| CCCAGACATG TAATACTCCT TAATTGGGAA GTCATCCATT CTTTCCCTTT CCCAAGTCCT | 2220 |
| TGCTTATTAA GAGGTTCAAG TCACCTACCC AATTCAGAAG CTTAAGTAAC CACTAACCAC | 2280 |
| CGTGACTGCG TGGGAGGCCT CCCATGGGCT GAGCTACTGA CTTGGCTTTG GGGGCCTTGG | 2340 |
| GCTGGGGCCC TCCTTAAAGC CCCCCCTGAA ATTGTCGGAC CTCAAAGTGT GACTCCTTTG | 2400 |
| AGTCTACTCG CCACCCCCGT GGCCCTTTGC AGCCCTGGTC CAGTCACCGA GGTACTGGA  | 2460 |
| AGTCCAGCTT GGATGGCCAG ACAGCTTTTT GGCACAGGCA GACCCATGCT CACCCAACAT | 2520 |
| TTTAGTGTC AGGTGCCCAG GTGCCCAGGT GCCCAGCTCC TGGGCATCAG ACAGTGGGAA  | 2580 |
| AGCTCCAGG ATCTACCATT CAGAGACTTC AGTTTGGATG TAGGGCTAAG GCCAGAGAAA  | 2640 |
| AGTCTGGAG CTTTTCATTT GGCCCAAGAA AAAACTGCCA AGATCCAGAA AAGTGGATCT  | 2700 |
| GAGTGGGAATT TAGATGCAAA GAGCTTGGAG                                 | 2730 |

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1869 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 77..1477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

|   |     |
|---|-----|
| CGAGTGGACA GTGGCAGGCG GTGACTGAAT CTCCAAGTCT GGAAACAATA GCCAGAGATA | 60  |
| GTGGCTGGGA AGCACCATGG CCAGAGTCCT GCAGCTCTCC CTGACTGCTC TCCTGCTGCC | 120 |

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| TGTGGCTATT | GCTATGCACT | CTGACTGCAT | CTTCAAGAAG | GAGCAAGCCA | TGTGCCTGGA | 180  |
| GAGGATCCAG | AGGGCCAACG | ACCTGATGGG | ACTAAACGAG | TCTTCCCCAG | GTTGCCCTGG | 240  |
| CATGTGGGAC | AATATCACAT | GTTGGAAGCC | AGCTCAAGTA | GGTGAGATGG | TCCTTGTAAG | 300  |
| CTGCCCTGAG | GTCTTCCGGA | TCTTCAACCC | GGACCAAGTC | TGGATGACAG | AAACCATAGG | 360  |
| AGATTCTGGT | TTTGCCGATA | GTAATTCCTT | GGAGATCACA | GACATGGGGG | TCGTGGGCCG | 420  |
| GAAGTGCACA | GAGGACGGCT | GGTCGGAGCC | CTTCCCCCAC | TACTTCGATG | CTTGTGGGTT | 480  |
| TGATGATTAT | GAGCCTGAGT | CTGGAGATCA | GGATTATTAC | TACCTGTCGG | TGAAGGCTCT | 540  |
| CTACACAGTC | GGCTACAGCA | CTTCCCTCGC | CACCCTCACT | ACTGCCATGG | TCATCTTGTC | 600  |
| CCGCTTCCGG | AAGCTGCATT | GCACTCGCAA | CTTCATCCAC | ATGAACCTGT | TTGTATCCTT | 660  |
| CATGCTGAGG | GCTATCTCCG | TCTTCATCAA | GGACTGGATC | TTGTACGCCG | AGCAGGACAG | 720  |
| CAGTCACTGC | TTCGTTTCCA | CCGTGGAGTG | CAAAGCTGTC | ATGGTTTTCT | TCCACTACTG | 780  |
| CGTGGTGTCC | AACTACTTCT | GGCTGTTTCA | TGAAGGCCTG | TACCTCTTTA | CACTGCTGGT | 840  |
| GGAGACCTTC | TTCCCTGAGA | GGAGATATTT | CTACTGGTAC | ACCATCATCG | GCTGGGGGAC | 900  |
| ACCTACTGTG | TGTGTAACAG | TGTGGGCTGT | GCTGAGGCTC | TATTTTGATG | ATGCAGGATG | 960  |
| CTGGGATATG | AATGACAGCA | CAGCTCTGTG | GTGGGTGATC | AAAGGCCCCG | TGGTTGGCTC | 1020 |
| TATAATGGTT | AACTTTGTGC | TTTTCATCGG | CATCATCATC | ATCCTTGATC | AGAAGCTGCA | 1080 |
| GTCCCCAGAC | ATGGGAGGCA | ACGAGTCCAG | CATCTACTTA | CGGCTGGCCC | GCTCCACCCT | 1140 |
| ACTGCTCATC | CCACTCTTCG | GAATCCACTA | CACAGTATTC | GCCTTCTCTC | CAGAGAACGT | 1200 |
| CAGCAAGAGG | GAAAGACTTG | TGTTTGAGCT | TGGGCTGGGC | TCCTTCCAGG | GCTTTGTGGT | 1260 |
| GGCTGTACTC | TACTGCTTCC | TGAATGGGGA | GGTACAGGCA | GAGATTAAGA | GGAAATGGAG | 1320 |
| GAGCTGGAAG | GTGAACCGTT | ACTTCACTAT | GGACTTCAAG | CACCGGCACC | CGTCCCTGGC | 1380 |
| CAGCAGTGA  | GTAAATGGGG | GAACCCAGCT | GTCCATCCTG | AGCAAGAGCA | GCTCCCAGCT | 1440 |
| CCGCATGTCC | AGCCTCCCCG | CCGACAACTT | GGCCACCTGA | GGCCTGTCTC | CCTCCTCCTT | 1500 |
| CTGCACAGGC | TGGGGCTGCG | GGCCAGTGCC | TGAGCATGTT | TGTGCCTCTC | CCCTCTCCTT | 1560 |
| GGGCAGGCCC | TGGGTAGGAA | GCTGGGCTCC | TCCCCAAAGG | GGAAGAGAGA | GATAGGGTAT | 1620 |
| AGGCTGATAT | TGCTCCTCCT | GTTTGGGTCC | CACCTACTGT | GATTCATTGA | GCCTGATTTG | 1680 |

|   |      |
|---|------|
| ACATGTAAAT ACACCTCAAA TTTGGAAAGT TGCCCCATCT CTGCCCCCAA CCCATGCCCC | 1740 |
| TGCTCACCTC TGCCAGGCCC CAGCTCAACC TACTGTGTCA AGGCCAGCCT CAGTGATAGT | 1800 |
| CTGATCCCAG GTACAAGGCC TTGTGAGCTG AGGCTGAAAG GCCTGTTTTG GAGAGGCTGG | 1860 |
| GGTAGTGCC   | 1869 |

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2548 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 77..1561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

|  |     |
|--|-----|
| CGAGTGGACA GTGGCAGGCG GTGACTGAAT CTCCAAGTCT GGAAACAATA GCCAGAGATA  | 60  |
| GTGGCTGGGA AGCACCATGG CCAGAGTCCT GCAGCTCTCC CTGACTGCTC TCCTGCTGCC  | 120 |
| TGTGGCTATT GCTATGCACT CTGACTGCAT CTTCAAGAAG GAGCAAGCCA TGTGCCTGGA  | 180 |
| GAGGATCCAG AGGGCCAACG ACCTGATGGG ACTAAACGAG TCTTCCCCAG GTTGCCCTGG  | 240 |
| CATGTGGGAC AATATCACAT GTTGGAAGCC AGCTCAAGTA GGTGAGATGG TECTTGTAAG  | 300 |
| CTGCCCTGAG GTCTTCCGGA TCTTCAACCC GGACCAAGTC TGGATGACAG AAACCATAGG  | 360 |
| AGATTCTGGT TTTGCCGATA GTAATTCCTT GGAGATCACA GACATGGGGG TCGTGGGCCG  | 420 |
| GAACTGCACA GAGGACGGCT GGTCCGAGCC CTTCCCCCAC TACTTCGATG CTTGTGGGTT  | 480 |
| TGATGATTAT GAGCCTGAGT CTGGAGATCA GGATTATTAC TACCTGTCGG TGAAGGCTCT  | 540 |
| CTACACAGTC GGCTACAGCA CTTCCCTCGC CACCCTCACT ACTGCCATGG TCATCTTGTT  | 600 |
| CCGCTTCCGG AAGCTGCATT GCACTCGCAA CTTTCATCCAC ATGAACCTGT TTGTATCCTT | 660 |
| CATGCTGAGG GCTATCTCCG TCTTCATCAA GGACTGGATC TTGTACGCCG AGCAGGACAG  | 720 |
| CAGTCACTGC TTCGTTTCCA CCGTGGAGTG CAAAGCTGTC ATGGTTTTCT TCCACTACTG  | 780 |

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| CGTGGTGTCC | AACTACTTCT | GGCTGTTCAT | TGAAGGCCTG | TACCTCTTTA | CACTGCTGGT | 840  |
| GGAGACCTTC | TTCCCTGAGA | GGAGATATTT | CTACTGGTAC | ACCATCATCG | GCTGGGGGAC | 900  |
| ACCTACTGTG | TGTGTAACAG | TGTGGGCTGT | GCTGAGGCTC | TATTTTGATG | ATGCAGGATG | 960  |
| CTGGGATATG | AATGACAGCA | CAGCTCTGTG | GTGGGTGATC | AAAGGCCCCG | TGGTTGGCTC | 1020 |
| TATAATGGTT | AACTTTGTGC | TTTTCATCGG | CATCATCATC | ATCCTTGTAC | AGAAGCTGCA | 1080 |
| GTCCCCAGAC | ATGGGAGGCA | ACGAGTCCAG | CATCTACTTC | AGCTGCGTGC | AGAAATGCTA | 1140 |
| CTGCAAGCCA | CAGCGGGCTC | AGCAGCACTC | TTGCAAGATG | TCAGAACTAT | CCACCATTAC | 1200 |
| TCTACGGCTG | GCCCGCTCCA | CCCTACTGCT | CATCCCACTC | TTCGGAATCC | ACTACACAGT | 1260 |
| ATTGCGCTTC | TCTCCAGAGA | ACGTCAGCAA | GAGGGAAAGA | CTTGTGTTTG | AGCTTGGGCT | 1320 |
| GGCTCCTTC  | CAGGGCTTTG | TGGTGGCTGT | ACTCTACTGC | TTCCTGAATG | GGGAGGTACA | 1380 |
| GGCAGAGATT | AAGAGGAAAT | GGAGGAGCTG | GAAGGTGAAC | CGTTACTTCA | CTATGGACTT | 1440 |
| CAAGCACCGG | CACCCGTCCC | TGGCCAGCAG | TGGAGTAAAT | GGGGGAACCC | AGCTGTCCAT | 1500 |
| CCTGAGCAAG | AGCAGCTCCC | AGCTCCGCAT | GTCCAGCCTC | CCGGCCGACA | ACTTGGCCAC | 1560 |
| CTGAGGCCTG | TCTCCCTCCT | CCTTCTGCAC | AGGCTGGGGC | TGCGGGCCAG | TGCCTGAGCA | 1620 |
| TGTTTGTC   | TCTCCCCTCT | CCTTGGGCAG | GCCCTGGGTA | GGAAGCTGGG | CTCCTCCCCA | 1680 |
| AAGGGGAAGA | GAGAGATAGG | GTATAGGCTG | ATATTGCTCC | TCCTGTTTGG | GTCCCACCTA | 1740 |
| CTGTGATTCA | TTGAGCCTGA | TTTGACATGT | AAATACACCT | CAAATTTGGA | AAGTTGCCCC | 1800 |
| ATCTCTGCCC | CCAACCCATG | CCCCTGCTCA | CCTCTGCCAG | GCCCCAGCTC | AACCTACTGT | 1860 |
| GTCAAGGCCA | GCCTCAGTGA | TAGTCTGATC | CCAGGTACAA | GGCCTTGTGA | GCTGAGGCTG | 1920 |
| AAAGGCCTGT | TTTGGAGAGG | CTGGGGTAGT | GCCCACCCCA | GCAGCCTTTC | AGCAAATTGA | 1980 |
| CTTTGGATGT | GGACCCTTCT | CAGCCTGTAC | CAAGTACTGC | AGTTGGCTAG | GGATGCAGCT | 2040 |
| CAGTTTCCTG | AGCATCCTTT | GGAGCAGGTC | AACCTGAGGC | TCCTTTTGCT | TACCCGACAT | 2100 |
| CTAAGTTGTC | CAGGTGCTCG | GCTCCTGTGT | GCCTGGATGA | CGGGAGGGCT | CCGGGGTCTT | 2160 |
| TCAGTCAAAG | ACTTACATTG | AGGTGGGGTG | AGAGTCAGAG | AAAAGTTCTG | GTGCTTTTCA | 2220 |
| TTTGTTCTAA | GAGCTGAGAG | CCAGGAATGC | AGAGTCAATT | GGAAGGAGA  | TGGGATAGCT | 2280 |
| GATGATCTTA | CCATGTCCAT | GACTGTGCCC | CTGATTCAAG | ACCGGATCAT | GTGGTGGCTT | 2340 |



TATTTCTACA CTTCTTGTCC ACAATGGACA GTCTGAGGAA GCTCTTCTTT CAGCCACAAC 2400  
 AACCACAGAA AGCCCTTTCT TCTCCCCTCT TGTTTCTCCA TAAGTCAAAG CCATGTTTAG 2460  
 AACGGACCAG CCACCTTGCG ATGAAATCAC TGAGTTCTGA AGCAACTTTC AATTTCCACG 2520  
 AGCCAAGTCC TGGGTCCAGG GACGCCCC 2548

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1664 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 74..1648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AGCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGCTG 60  
 GCCAAGAAGT GTCATGGCTG GTGTCGTGCA CGTTTCCCTG GCTGCTCACT GCGGGGCCTG 120  
 TCCGTGGGGC CGGGGCAGAC TCCGCAAAGG ACGCGCAGCC TGCAAGTCCG CGGCCAGAG 180  
 ACACATTGGG GCTGACCTGC CGCTGCTGTC AGTGGGAGGC CAGTGGTGCT GGCCAAGAAG 240  
 TGTCATGGCT GGTGTCGTGC ACGTTTCCCT GGCTGCTCTC CTCCTGCTGC CTATGGCCCC 300  
 TGCCATGCAT TCTGACTGCA TCTTCAAGAA GGAGCAAGCC ATGTGCCTGG AGAAGATCCA 360  
 GAGGGCCAAT GAGCTGATGG GCTTCAATGA TTCCTCTCCA GGCTGTCCTG GGATGTGGGA 420  
 CAACATCACG TGTTGGAAGC CCGCCCATGT GGGTGAGATG GTCCTGGTCA GCTGCCCTGA 480  
 GCTCTTCCGA ATCTTCAACC CAGACCAAGT CTGGGAGACC GAAACCATTG GAGAGTCTGA 540  
 TTTTGGTGAC AGTAACTCCT TAGATCTCTC AGACATGGGA GTGGTGAGCC GGAAGTGCAC 600  
 GGAGGATGGC TGGTCGGAAC CCTTCCCTCA TTAATTTGAT GCCTGTGGGT TTGATGAATA 660  
 TGAATCTGAG ACTGGGGACC AGGATTATTA CTACCTGTCA GTGAAGGCCC TCTACACGGT 720  
 TGGCTACAGC ACATCCCTCG TCACCCTCAC CACTGCCATG GTCATCCTTT GTCGCTTCCG 780

|   |      |
|---|------|
| GAAGCTGCAC TGCACACGCA ACTTCATCCA CATGAACCTG TTTGTGTCGT TCATGCTGAG   | 840  |
| GGCGATCTCC GTCTTCATCA AAGACTGGAT TCTGTATGCG GAGCAGGACA GCAACCACTG   | 900  |
| CTTCATCTCC ACTGTGGAAT GTAAGGCCGT CATGGTTTTTTC TTCCACTACT GTGTTGTGTC | 960  |
| CAACTACTTC TGGCTGTTCA TCGAGGGCCT GTACCTCTTC ACTCTGCTGG TGGAGACCTT   | 1020 |
| CTTCCCTGAA AGGAGATACT TCTACTGGTA CACCATCATT GGCTGGGGGT CCCCAACTGT   | 1080 |
| GTGTGTGACA GTGTGGGCTA CGCTGAGACT CTACTTTGAT GACACAGGCT GCTGGGATAT   | 1140 |
| GAATGACAGC ACAGCTCTGT GGTGGGTGAT CAAAGGCCCT GTGGTTGGCT CTATCATGGT   | 1200 |
| TAACCTTTGTG CTTTTTATTG GCATTATCGT CATCCTTGTG CAGAACTTC AGTCTCCAGA   | 1260 |
| CATGGGAGGC AATGAGTCCA GCATCTACTT GCGACTGGCC CGGTCCACCC TGCTGCTCAT   | 1320 |
| CCCCTATTTC GGAATCCACT ACACAGTATT TGCCTTCTCC CCAGAGAATG TCAGCAAAAG   | 1380 |
| GGAAAGACTC GTGTTTGAGC TGGGGCTGGG CTCCTTCCAG GGCTTTGTGG TGGCTGTTCT   | 1440 |
| CTACTGTTTT CTGAATGGTG AGGTACAAGC GGAGATCAAG CGAAAATGGC GAAGCTGGAA   | 1500 |
| GGTGAACCGT TACTTCGCTG TGGACTTCAA GCACCGACAC CCGTCTCTGG CCAGCAGTGG   | 1560 |
| GGTGAATGGG GGCACCCAGC TCTCCATCCT GAGCAAGAGC AGCTCCCAA TCCGCATGTC    | 1620 |
| TGGCCTCCCT GCTGACAATC TGGCCACCTG AGCCATGCTC CCCT                    | 1664 |

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 74..1732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

|  |     |
|--|-----|
| AGCCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGCTG  | 60  |
| GCCAAGAAGT GTCATGGCTG GTGTCGTGCA CGTTTCCCTG GCTGCTCACT GCGGGGCCCTG | 120 |

|            |            |            |             |            |            |      |
|------------|------------|------------|-------------|------------|------------|------|
| TCCGTGGGGC | CGGGGCAGAC | TCCGCAAAGG | ACGCGCAGCC  | TGCAAGTCCG | CGGCCCAGAG | 180  |
| ACACATTGGG | GCTGACCTGC | CGCTGCTGTC | AGTGGGAGGC  | CAGTGGTGCT | GGCCAAGAAG | 240  |
| TGTCATGGCT | GGTGTCTGTC | ACGTTTCCCT | GGCTGCTCTC  | CTCCTGCTGC | CTATGGCCCC | 300  |
| TGCCATGCAT | TCTGACTGCA | TCTTCAAGAA | GGAGCAAGCC  | ATGTGCCTGG | AGAAGATCCA | 360  |
| GAGGGCCAAT | GAGCTGATGG | GCTTCAATGA | TTCCTCTCCA  | GGCTGTCCTG | GGATGTGGGA | 420  |
| CAACATCACG | TGTTGGAAGC | CCGCCCATGT | GGGTGAGATG  | GTCCTGGTCA | GCTGCCCTGA | 480  |
| GCTCTTCCGA | ATCTTCAACC | CAGACCAAGT | CTGGGAGACC  | GAAACCATTG | GAGAGTCTGA | 540  |
| TTTTGGTGAC | AGTAACTCCT | TAGATCTCTC | AGACATGGGA  | GTGGTGAGCC | GGAAGTGCAC | 600  |
| GGAGGATGGC | TGGTCGGAAC | CCTTCCCTCA | TTACTTTGAT  | GCCTGTGGGT | TTGATGAATA | 660  |
| TGAATCTGAG | ACTGGGGACC | AGGATTATTA | CTACCTGTCA  | GTGAAGGCCC | TCTACACGGT | 720  |
| TGGCTACAGC | ACATCCCTCG | TCACCCTCAC | CACTGCCATG  | GTCATCCTTT | GTCGCTTCCG | 780  |
| GAAGCTGCAC | TGCACACGCA | ACTTCATCCA | CATGAACCTG  | TTTGTGTCGT | TCATGCTGAG | 840  |
| GGGATCTCC  | GTCTTCATCA | AAGACTGGAT | TCTGTATGCG  | GAGCAGGACA | GCAACCACTG | 900  |
| CTTCATCTCC | ACTGTGGAAT | GTAAGGCCGT | CATGGTTTTT  | TTCCACTACT | GTGTTGTGTC | 960  |
| CAACTACTTC | TGGCTGTTCA | TCGAGGGCCT | GTACCTCTTC  | ACTCTGCTGG | TGGAGACCTT | 1020 |
| CTTCCCTGAA | AGGAGATACT | TCTACTGGTA | CACCATCATT  | GGCTGGGGGA | CCCCAACTGT | 1080 |
| GTGTGTGACA | GTGTGGGCTA | CGCTGAGACT | CTACTTTGAT  | GACACAGGCT | GCTGGGATAT | 1140 |
| GAATGACAGC | ACAGCTCTGT | GGTGGGTGAT | CAAAGGCCCT  | GTGGTTGGCT | CTATCATGGT | 1200 |
| TAACTTTGTG | CTTTTTATTG | GCATTATCGT | CATCCTTG TG | CAGAAACTTC | AGTCTCCAGA | 1260 |
| CATGGGAGGC | AATGAGTCCA | GCATCTACTT | CAGCTGCGTG  | CAGAAATGCT | ACTGCAAGCC | 1320 |
| ACAGCGGGCT | CAGCAGCACT | CTTGCAAGAT | GTCAGAACTG  | TCCACCATTA | CTCTGCGACT | 1380 |
| GGCCCGGTCC | ACCCTGCTGC | TCATCCCACT | ATTCGGAATC  | CACTACACAG | TATTTGCCTT | 1440 |
| CTCCCCAGAG | AATGTCAGCA | AAAGGGAAAG | ACTCGTGTTT  | GAGCTGGGGC | TGGGCTCCTT | 1500 |
| CCAGGGCTTT | GTGGTGGCTG | TTCTCTACTG | TTTTCTGAAT  | GGTGAGGTAC | AAGCGGAGAT | 1560 |
| CAAGCGAAAA | TGGCGAAGCT | GGAAGGTGAA | CCGTTACTTC  | GCTGTGGACT | TCAAGCACCG | 1620 |
| ACACCCGTCT | CTGGCCAGCA | GTGGGGTGAA | TGGGGGCACC  | CAGCTCTCCA | TCCTGAGCAA | 1680 |

GAGCAGCTCC CAAATCCGCA TGTCTGGCCT CCCTGCTGAC AATCTGGCCA CCTGAGCCAT 1740  
 GCTCCCCT 1748

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1745 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 74..1729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

AGCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGCTG 60  
 GCCAAGAAGT GTCATGGCTG GTGTCGTGCA CGTTTCCCTG GCTGCTCACT GCGGGGCCTG 120  
 TCCGTGGGGC CGGGGCAGAC TCCGCAAAGG ACGCGCAGCC TGCAAGTCCG CGGCCAGAG 180  
 ACACATTGGG GCTGACCTGC CGCTGCTGTC AGTGGGAGGC CAGTGGTGCT GGCCAAGAAG 240  
 TGTGATGGCT GGTGTCGTGC ACGTTTCCCT GGCTGCTCTC CTCCTGCTGC CTATGGCCCC 300  
 TGCCATGCAT TCTGACTGCA TCTTCAAGAA GGAGCAAGCC ATGTGCCTGG AGAAGATCCA 360  
 GAGGGCCAAT GAGCTGATGG GCTTCAATGA TTCCTCTCCA GGCTGTCCTG GGATGTGGGA 420  
 CAACATCACG TGTTGGAAGC CCGCCCATGT GGGTGAGATG GTCCTGGTCA GCTGCCCTGA 480  
 GCTCTTCCGA ATCTTCAACC CAGACCAAGT CTGGGAGACC GAAACCATTG GAGAGTCTGA 540  
 TTTTGGTGAC AGTAACTCCT TAGATCTCTC AGACATGGGA GTGGTGAGCC GGAAGTGCAC 600  
 GGAGGATGGC TGGTCGGAAC CCTTCCCTCA TTACTTTGAT GCCTGTGGGT TTGATGAATA 660  
 TGAATCTGAG ACTGGGGACC AGGATTATTA CTACCTGTCA GTGAAGGCC TCTACACGGT 720  
 TGGCTACAGC ACATCCCTCG TCACCCTCAC CACTGCCATG GTCATCCTTT GTCGCTTCCG 780  
 GAAGCTGCAC TGCACACGCA ACTTCATCCA CATGAACCTG TTTGTGTCGT TCATGCTGAG 840  
 GGCGATCTCC GTCTTCATCA AAGACTGGAT TCTGTATGCG GAGCAGGACA GCAACCACTG 900

CTTCATCTCC ACTGTGGAAT GTAAGGCCGT CATGGTTTTTTC TTCCACTACT GTGTTGTGTC 960  
 CAACTACTTC TGGCTGTTCA TCGAGGGCCT GTACCTCTTC ACTCTGCTGG TGGAGACCTT 1020  
 CTTCCCTGAA AGGAGATACT TCTACTGGTA CACCATCATT GGCTGGGGGA CCCCAACTGT 1080  
 GTGTGTGACA GTGTGGGCTA CGCTGAGACT CTACTTTGAT GACACAGGCT GCTGGGATAT 1140  
 GAATGACAGC ACAGCTCTGT GGTGGGTGAT CAAAGGCCCT GTGGTTGGCT CTATCATGGT 1200  
 TAACTTTGTG CTTTTTATTG GCATTATCGT CATCCTTGTG CAGAACTTC AGTCTCCAGA 1260  
 CATGGGAGGC AATGAGTCCA GCATCTACTT CTGCGTGCAG AAATGCTACT GCAAGCCACA 1320  
 GCGGGCTCAG CAGCACTCTT GCAAGATGTC AGAACTGTCC ACCATTACTC TCGGACTGGC 1380  
 CCGGTCCACC CTGCTGCTCA TCCCCTATT CGGAATCCAC TACACAGTAT TTGCCTTCTC 1440  
 CCCAGAGAAT GTCAGCAAAA GGGAAAGACT CGTGTTTGAG CTGGGGCTGG GCTCCTTCCA 1500  
 GGGCTTTGTG GTGGCTGTTC TCTACTGTTT TCTGAATGGT GAGGTACAAG CGGAGATCAA 1560  
 GCGAAAATGG CGAAGCTGGA AGGTGAACCG TTAATTTCGCT GTGGACTTCA AGCACCGACA 1620  
 CCCGTCTCTG GCCAGCAGTG GGGTGAATGG GGGCACCCAG CTCTCCATCC TGAGCAAGAG 1680  
 CAGCTCCCAA ATCCGCATGT CTGGCCTCCC TGCTGACAAT CTGGCCACCT GAGCCATGCT 1740  
 CCCCT 1745

## (2) INFORMATION FOR SEQ ID NO:45:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 74..1732

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AGCCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGCTG 60  
 GCCAAGAAGT GTCATGGCTG GTGTCGTGCA CGTTTCCCTG GCTGCTCACT GCGGGGCCTG 120

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| TCCGTGGGGC | CGGGGCAGAC | TCCGCAAAGG | ACGCGCAGCC | TGCAAGTCCG | CGGCCCAGAG | 180  |
| ACACATTGGG | GCTGACCTGC | CGCTGCTGTC | AGTGGGAGGC | CAGTGGTGCT | GGCCAAGAAG | 240  |
| TGTCATGGCT | GGTGTCTGTC | ACGTTTCCCT | GGCTGCTCTC | CTCCTGCTGC | CTATGGCCCC | 300  |
| TGCCATGCAT | TCTGACTGCA | TCTTCAAGAA | GGAGCAAGCC | ATGTGCCTGG | AGAAGATCCA | 360  |
| GAGGGCCAAT | GAGCTGATGG | GCTTCAATGA | TTCCTCTCCA | GGCTGTCCTG | GGATGTGGGA | 420  |
| CAACATCACG | TGTTGGAAGC | CCGCCCATGT | GGGTGAGATG | GTCCTGGTCA | GCTGCCCTGA | 480  |
| GCTCTTCCGA | ATCTTCAACC | CAGACCAAGT | CTGGGAGACC | GAAACCATTG | GAGAGTCTGA | 540  |
| TTTTGGTGAC | AGTAACTCCT | TAGATCTCTC | AGACATGGGA | GTGGTGAGCC | GGAAGTGCAC | 600  |
| GGAGGATGGC | TGGTCGGAAC | CCTTCCCTCA | TTACTTTGAT | GCCTGTGGGT | TTGATGAATA | 660  |
| TGAATCTGAG | ACTGGGGACC | AGGATTATTA | CTACCTGTCA | GTGAAGGCC  | TCTACACGGT | 720  |
| TGGCTACAGC | ACATCCCTCG | TCACCCTCAC | CACTGCCATG | GTCATCCTTT | GTCGCTTCCG | 780  |
| GAAGCTGCAC | TGCACACGCA | ACTTCATCCA | CATGAACCTG | TTTGTGTCGT | TCATGCTGAG | 840  |
| GGGATCTCC  | GTCTTCATCA | AAGACTGGAT | TCTGTATGCG | GAGCAGGACA | GCAACCACTG | 900  |
| CTTCATCTCC | ACTGTGGAAT | GTAAGGCCGT | CATGGTTTTT | TTCCACTACT | GTGTTGTGTC | 960  |
| CAACTACTTC | TGGCTGTTCA | TCGAGGGCCT | GTACCTCTTC | ACTCTGCTGG | TGGAGACCTT | 1020 |
| CTTCCCTGAA | AGGAGATACT | TCTACTGGTA | CACCATCATT | GGCTGGGGGA | CCCCAACTGT | 1080 |
| GTGTGTGACA | GTGTGGGCTA | CGCTGAGACT | CTACTTTGAT | GACACAGGCT | GCTGGGATAT | 1140 |
| GAATGACAGC | ACAGCTCTGT | GGTGGGTGAT | CAAAGGCCCT | GTGGTTGGCT | CTATCATGGT | 1200 |
| TAACTTTGTG | CTTTTTATTG | GCATTATCGT | CATCCTTGTG | CAGAACTTC  | AGTCTCCAGA | 1260 |
| CATGGGAGGC | AATGAGTCCA | GCATCTACTT | AACAAATTTA | AGCCCGCGAG | TCCCCAAGAA | 1320 |
| AGCCCGAGAG | GACCCCCTGC | CTGTGCCCTC | AGACCAGCAT | TACTCCCTT  | TCCTGCGACT | 1380 |
| GGCCCGGTCC | ACCCTGCTGC | TCATCCCACT | ATTCGGAATC | CACTACACAG | TATTTGCCTT | 1440 |
| CTCCCCAGAG | AATGTCAGCA | AAAGGGAAAG | ACTCGTGTTT | GAGCTGGGGC | TGGGCTCCTT | 1500 |
| CCAGGGCTTT | GTGGTGGCTG | TTCTCTACTG | TTTTCTGAAT | GGTGAGGTAC | AAGCGGAGAT | 1560 |
| CAAGCGAAAA | TGGCGAAGCT | GGAAGGTGAA | CCGTTACTTC | GCTGTGGACT | TCAAGCACCG | 1620 |
| ACACCCGTCT | CTGGCCAGCA | GTGGGGTGAA | TGGGGGCACC | CAGCTCTCCA | TCCTGAGCAA | 1680 |

GAGCAGCTCC CAAATCCGCA TGTCTGGCCT CCCTGCTGAC AATCTGGCCA CCTGAGCCAT 1740  
GCTCCCCT 1748

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

His Ser Asp Gly Ile Phe Thr Asp Ser Tyr Ser Arg Tyr Arg Lys Gln  
1 5 10 15  
Met Ala Val Lys Lys Tyr Leu Ala Ala Val Leu Gly Lys Arg Tyr Lys  
20 25 30  
Gln Arg Val Lys Asn Lys  
35

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

His Ser Asp Gly Ile Phe Thr Asp Ser Tyr Ser Arg Tyr Arg Lys Gln  
1 5 10 15  
Met Ala Val Lys Lys Tyr Leu Ala Ala Val Leu  
20 25

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid, Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CAGAAAGCTT CGGACCATGC GCCCTCCGAG CCCACCG

37

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid, Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGGCTCTAGA CGGTCAGACC AGGGAGACCT CCGCTTG

37

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Cys | Ile | Phe | Lys | Lys | Glu | Gln | Ala | Met | Cys | Leu | Glu | Lys | Ile | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid, Synthetic DNA



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TGGATCTTCT CCAGGTGCAT DGCCTGCTCC TTCTTGAAGA TGTGGTC

47

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid, Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CTGGGATATG AATGACAGCA CAGC

24

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid, Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TCTGGGGAGA AGGCAAATAC TGTG

24

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid, Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TGCGTGCAGA AATGCTACTG CAAGCCACAG

30

